

CC treating or preventing breast cancer. The methods use sensitive and
 CC specific biomarkers provide early diagnosis of breast cancer, and the
 CC compositions are more potent, specific, and has a more rapid effect with
 CC fewer side effects than other prior art methods. The present sequence is
 CC a tryptic digest peptide from a BPI of the invention
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 Db 4 NMVPPFR 10
 |||||

RESULT 2
 AAE11786
 ID AAE11786 standard; peptide; 10 AA.
 XX
 AC AAE11786;

XX 18-DEC-2001 (first entry)

XX Native tubulin-beta-3-chain tryptic peptide 19.

XX Tubulin-beta-3 chain; peptide map; mass spectrometry; diagnostic;
 KW pharmaceutical; finger printing; tryptic peptide.
 KW
 XX Unidentified.

XX WO200157519-A2.

XX 09-AUG-2001.

XX 07-FEB-2001; 2001WO-EP001332.

XX 07-FEB-2000; 2000EP-00102567.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Cahill DJ, Nordhoff E, Klose J, Bickhoff H, Schmidt F, Lehrach H;

XX WPI; 2001-611112/70.

XX Identifying and/or characterizing peptide, comprises analyzing peptide
 PT map containing peptide and its primary structure fingerprint by mass
 PT spectrometry, and comparing obtained data with reference database.

XX Disclosure; Page 33; 55pp; English.

XX The invention relates to a method for identifying and/or characterising a
 CC polypeptide. The method involves analysing a peptide map of at least one
 CC peptide and its primary structure fingerprint by mass spectrometry and
 CC comparing the obtained data with a reference database. The method is
 CC useful for identification and/or characterisation of a polypeptide. The
 CC method is useful for applications where it is desired or needed to have
 CC direct access to the genetic information encoding the polypeptide the
 CC minimal protein identifiers of which has been found in the database. The
 CC method is also useful for the development of pharmaceuticals and/or
 CC diagnostics. The present sequence is native tubulin-beta-3-chain tryptic
 CC peptide used in the invention
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 Db 4 NMVPPFR 10
 |||||

RESULT 3
 ABP61745
 ID ABP61745 standard; peptide; 10 AA.
 XX
 AC ABP61745;
 XX
 DT 02-OCT-2002 (first entry)
 DE Human KRPI tryptic digest peptide #131.
 XX

XX Human; tryptic digest peptide; KRPI; kidney response; KR;
 KW nephrotropic kidney response-associated protein isoform; gene therapy;
 KW antisenese therapy; kidney function; tubular nephritis; renal failure;
 KW nephron cell metabolic pathway modulation; glomerular necrosis;
 KW papillary necrosis.
 XX

OS Homo sapiens.

XX WO200254081-A2.

XX 11-JUL-2002.

XX 24-DEC-2001; 2001WO-GB005777.

XX 29-DEC-2000; 2000US-0260392P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Holt GD, Kelly MD, Kennedy SJ, Moyses C;

XX WPI; 2002-593637/82.

XX Screening, diagnosis or prognosis of kidney response in subject, by
 PT detecting kidney response-associated features or kidney response-
 PT associated protein isoforms in body fluid or tissue from subject.

XX Disclosure; Page 46; 169pp; English.

XX The invention relates to a novel method for the screening, diagnosis or
 CC prognosis of kidney response (KR). The method of the invention has
 CC nephrotropic activity, and may have a use in gene therapy or antisenese
 CC therapy. The method is useful for the screening, diagnosis or prognosis
 CC of KR in a subject, for determining the stage or severity of KR in a
 CC subject, for identifying a subject at risk of developing KR, or for
 CC monitoring the effect of therapy administered to a subject with KR. An
 CC alternative method of the invention is useful for screening agents that
 CC interact with one or more of the kidney response-associated protein
 CC isoforms (KRPIs). The kidney response includes alterations in kidney
 CC function, any phase of nephron cell metabolic pathway modulation,
 CC glomerular/proximal tubular nephritis, glomerular/papillary necrosis,
 CC acute and chronic renal failure, and end stage renal disease. The
 CC sequences shown in ABP61514-ABP61787 represent tryptic digest peptides of
 CC the KRPIs of the invention
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 Db 4 NMVPPFR 10
 |||||

RESULT 4
 ABG67684
 ID ABG67684 standard; peptide; 10 AA.
 XX
 AC ABG67684;

DT 07-OCT-2002 (first entry)
 XX Human ADPI tryptic digest peptide #393.
 DE Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
 KW Alzheimer's disease-associated feature; neuroprotective;
 KW Alzheimer's disease-associated protein isoform; nontropic;
 KW ADPI tryptic digest peptide.
 XX Homo sapiens.
 OS WO200246767-A2.
 XX 13-JUN-2002.
 XX 29-NOV-2001; 2001WO-GB005289.
 XX 08-DEC-2000; 2000US-0254431P.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Herath HMAC, Parekh RB, Rohlf C;
 PI WPI; 2002-508575/54.
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprises detecting Alzheimer disease-associated features or Alzheimer
 PT disease-associated protein isoforms in brain tissue from the subject.
 XX Claim 7; Page 53; 427pp; English.
 CC The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
 CC subject. The method comprises analysing a sample of brain tissue from a
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
 CC disease-associated features (ADFs), whose relative abundance correlates
 CC with the presence, absence, stage or severity of AD and comparing the
 CC abundance of each feature with the abundance of that chosen feature in
 CC brain tissue from persons free from AD. The invention also describes
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
 CC brain tissue. The methods and compositions of the invention are useful
 CC for the screening, diagnosis or prognosis of AD in a subject, for
 CC determining the stage or severity of AD in a subject, for identifying a
 CC subject at risk of developing AD, or for monitoring the effect of therapy
 CC administered to a subject having AD. Antibodies capable of binding to
 CC ADPIs are useful for treating or preventing AD, and for determining the
 CC efficacy of a given treatment regime. An agent that modulates the
 CC activity of ADPI is useful in the manufacture of a medicament for the
 CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
 CC human ADPI tryptic digest peptides
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 40; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NMVPFPR 7
 Db |||||
 4 NMVPFPR 10
 RESULT 5
 ABP99008
 ID ABP99008 standard; peptide; 10 AA.
 AC ABP99008;
 XX 18-MAR-2003 (first entry)
 DT ErbB2 cell overexpression EOPI-14 peptide SEQ ID NO:140.
 DE ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;
 KW ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;

KW EOPI; EOF; ErbB2 overexpression feature; cytostatic; vaccine;
 KW gene therapy.
 OS Homo sapiens.
 XX WO200290991-A2.
 XX 14-NOV-2002.
 XX 02-MAY-2002; 2002WO-GB002047.
 XX 03-MAY-2001; 2001GB-00010886.
 XX 23-NOV-2001; 2001GB-00028183.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Herath HMAC, Page MJ;
 PI WPI; 2003-103531/09.
 XX Diagnosing and treating ErbB2-related cancer, comprises generating ErbB2
 PT Overexpression Features (EOFs) from test samples from a subject by
 PT electrophoresis, and comparing the EOFs in the sample with a
 PT predetermined reference range.
 XX Claim 3; Page 18; 106pp; English.
 CC The present invention describes a method for screening or diagnosing
 CC ErbB2-related cancer. The method comprises generating ErbB2
 CC overexpression features (EOFs) from test samples of body fluid from the
 CC subject by electrophoresis, and comparing the EOFs in the test sample
 CC with that from normal subjects or with an expression reference feature
 CC (ERF) in the test sample. Also described: (1) an antibody capable of
 CC immunospecific binding to an ErbB2 overexpression protein isoform (EOPI);
 CC (2) pharmaceutical compositions comprising an EOPI, a nucleic acid
 CC encoding an EOPI, an amount of the above antibody or its fragment, and a
 CC carrier; (3) a kit comprising one or more antibodies and/or EOPIs cited
 CC above, other reagents and instructions for use; (4) methods of treating
 CC or preventing ErbB2-related cancer; (5) methods of screening for or
 CC identifying agents that interact with or modulate the expression or
 CC activity of, one or more EOPIs, EOPI fragment, EOPI-related polypeptides,
 CC or EOPI-fusion proteins; (6) a method for modulating the activity of one
 CC or more of the ErbB2 EOPIs, comprising administering to a subject an
 CC agent identified by the method of (5); and (7) a method for identifying
 CC targets for therapeutic modulation of ErbB2-related cancer. EOPIs have
 CC cytostatic activity and can be used in vaccines and gene therapy. The
 CC method is useful in screening, diagnosing, preventing or treating ErbB2-
 CC related cancer, determining the stage or severity of ErbB2-related
 CC cancer, identifying a subject at risk of developing ErbB2-related cancer,
 CC monitoring the effect of therapy administered to a subject with ErbB2-
 CC related cancer, and for drug screening or drug development. The kit is
 CC useful in carrying out the above methods. ABP98940 to ABP99206 represent
 CC specifically claimed EOPIs from the present invention
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 40; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NMVPFPR 7
 Db |||||
 4 NMVPFPR 10
 RESULT 6
 ADA24202
 ID ADA24202 standard; peptide; 10 AA.
 XX ADA24202;
 AC ADA24202;
 XX 20-NOV-2003 (first entry)
 DT ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;
 KW ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;

DE Alzheimer's disease-associated protein isoform tryptic peptide #807.
XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
XX US2003064411-A1.
XX
XX 03-APR-2003.
XX
XX 10-DEC-2001; 2001US-00014340.
XX
XX 08-DEC-2000; 2000US-0254431P.
XX
XX (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
XX WPI; 2003-540784/51.
XX
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 807; 115pp; English.
XX
XX The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potentially, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 40; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Indels 0; Gaps 0;
QY 1 NMVPPFR 7
DB 4 NMVPPFR 10
RESULT 7
ADA23813
ID ADA23813 standard; peptide; 10 AA.
XX
XX ADA23813;
AC
XX 1 NMVPPFR 7
DB 4 NMVPPFR 10
20-NOV-2003 (first entry)
XX
XX Alzheimer's disease-associated protein isoform tryptic peptide #422.
DE human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
XX Homo sapiens.
OS
XX

PN US2003064411-A1.
XX
XX 03-APR-2003.
XX
XX 10-DEC-2001; 2001US-00014340.
XX
XX 08-DEC-2000; 2000US-0254431P.
XX
XX (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAC, Parekh RB, Rohlf C;
XX
XX WPI; 2003-540784/51.
XX
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 422; 115pp; English.
XX
XX The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potentially, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 40; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Indels 0; Gaps 0;
QY 1 NMVPPFR 7
DB 4 NMVPPFR 10
RESULT 8
ADA23814
ID ADA23814 standard; peptide; 10 AA.
XX
XX ADA23814;
AC
XX 1 NMVPPFR 7
DB 4 NMVPPFR 10
20-NOV-2003 (first entry)
XX
XX Alzheimer's disease-associated protein isoform tryptic peptide #423.
DE human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
XX Homo sapiens.
OS
XX
XX US2003064411-A1.
XX
XX 03-APR-2003.
XX
XX 10-DEC-2001; 2001US-00014340.
XX
XX 08-DEC-2000; 2000US-0254431P.
XX

PA (HERA//) HERATH H M A C.
 PA (PARE//) PAREKH R B.
 PA (ROHL//) ROHLFF C.
 XX
 PI Herath HMac, Parekh RB, Rohlf C;
 XX
 DR WPI; 2003-540784/51.
 XX
 XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT involves analyzing test sample of brain tissue from subject, and
 PT comparing feature in test sample with that of person(s) free from
 PT Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 423; 115pp; English.
 XX
 CC The invention relates to a method of screening or diagnosing Alzheimer's
 CC disease in a subject. The method is useful for screening, diagnosis or
 CC prognosis of Alzheimer's disease in a subject for determining the stage
 CC of severity of Alzheimer's disease in a subject, for identifying a
 CC subject at risk of developing Alzheimer's disease, or for monitoring the
 CC effect of therapy administered to a subject having Alzheimer's disease.
 CC The method is also useful in treating vascular dementia, Lewy body
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
 CC depression. The inventive method identifies sensitive and specific
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
 CC It provides therapeutic agents for Alzheimer's disease that works
 CC quickly, potentially, specifically with fewer side effects. The present
 CC sequence represents the amino acid sequence of a Alzheimer's disease-
 CC associated protein isoform tryptic peptide.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NMVPFPR 7
 Db |||||
 4 NMVPFPR 10
 RESULT 9
 ID AAM14569 standard; protein; 199 AA.
 XX
 AC AAM14569;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Peptide #1003 encoded by probe for measuring cervical gene expression.
 XX
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX
 OS Homo sapiens.
 XX
 EN WO200157278-A2.
 XX
 FD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 FA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 27; SEQ ID NO 19395; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SNP; see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SNPs are derived from human HeLa cells. The SNPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 199 AA;
 Query Match 100.0%; Score 40; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NMVPFPR 7
 Db |||||
 34 NMVPFPR 40
 RESULT 10
 ABB33529
 ID ABB33529 standard; peptide; 199 AA.
 XX
 AC ABB33529;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #1035 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 EN WO200157277-A2.
 XX
 FD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 FA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX
 PS Claim 27; SEQ ID NO 26164; 639pp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 199 AA;

Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|||||
Db 34 NMVPFPR 40

RESULT 11

AAM26989
ID AAM26989 standard; protein; 199 AA.

XX AC AAM26989;

XX DT 17-OCT-2001 (first entry)

XX DE Peptide #1026 encoded by probe for measuring placental gene expression.

XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.

XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P;

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.

XX PS Claim 27; SEQ ID NO 27258; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENP;
XX see AA13115-AA157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders

XX SQ Sequence 199 AA;

Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|||||
Db 34 NMVPFPR 40

RESULT 12

ABB28350
ID ABB28350 standard; peptide; 199 AA.

XX AC ABB28350;

XX DT 01-FEB-2002 (first entry)

XX DE Peptide #1001 encoded by breast cell single exon nucleic acid probe.

XX KW Human; microarray; single exon probe; gene expression; breast; disease;
XX cancer.

XX OS Homo sapiens.

XX PN WO200157271-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000662.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-496933/54.

XX PT New spatially-addressable set of single exon nucleic acid probes, useful
XX for measuring gene expression in sample derived from human breast,
XX comprises number of single exon nucleic acid probes.

XX PS Claim 27; SEQ ID NO 11318; 327pp + Sequence Listing; English.

XX CC The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosing breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a peptide
XX encoded by a single exon nucleic acid probe of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 199 AA;

Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|||||
Db 34 NMVPFPR 40

RESULT 13

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ABB18986
ID ABB18986 standard; protein; 199 AA.
XX AC ABB18986;
XX DT 23-JAN-2002 (first entry)
XX DE Protein #985 encoded by probe for measuring heart cell gene expression.
XX KW Human; gene expression; heart; microarray; vascular system;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488990/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 15; SEQ ID NO 20756; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart (see
XX CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX CC probe. The probes may be used for predicting, measuring and displaying
XX CC gene expression in samples derived from the human heart via microarrays.
XX CC By measuring gene expression, the probes are useful for predicting,
XX CC diagnosing, grading, staging, monitoring and prognosing diseases of the
XX CC human heart and vascular system e.g. cardiovascular disease,
XX CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 199 AA;

Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 34 NMVPPFR 40
|||||
|||||

RESULT 14
AAM66703
ID. AAM66703 standard; protein; 199 AA.
XX AC AAM66703;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27009.

Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 34 NMVPPFR 40
|||||
|||||

RESULT 15
AAM54306
ID AAM54306 standard; protein; 199 AA.
XX AC AAM54306;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26411.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.

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XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488990/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 27009; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention
XX SQ Sequence 199 AA;

Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 34 NMVPPFR 40
|||||
|||||

RESULT 15
AAM54306
ID AAM54306 standard; protein; 199 AA.
XX AC AAM54306;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26411.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.

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PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX Example 4; SEQ ID NO 26411; 650pp +. Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 199 AA;
Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NMVPFPR 7
Db 34 NMVPFPR 40
|||||
RESULT 16
ABG48373
ID ABG48373 standard; peptide; 199 AA.
XX
AC ABG48373;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID NO 27021.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.

PS Claim 27; SEQ ID NO 27021; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 199 AA;
Query Match 100.0%; Score 40; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NMVPFPR 7
Db 34 NMVPFPR 40
|||||
RESULT 17
AAM02295
ID AAM02295 standard; protein; 199 AA.
XX
AC AAM02295;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #977 encoded by probe for measuring human breast gene expression.
XX
KW Probe; human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US000661.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
XX
PS Claim 27; SEQ ID NO 11035; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AA100010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for

CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer, disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative
 CC breast disease and non-carcinoma tumours. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 199 AA;
 CC
 CC Query Match 100.0%; Score 40; DB 4; Length 199;
 CC Best Local Similarity 100.0%; Pred. No. 5;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 NMVPPPR 7
 CC Db 34 NMVPPPR 40
 CC
 CC RESULT 18
 CC ABG36358
 CC ID ABG36358 standard; peptide; 199 AA.
 CC XX
 CC AC ABG36358;
 CC XX
 CC DT 19-AUG-2002 (first entry)
 CC DE
 CC Human peptide encoded by genome-derived single exon probe SEQ ID 26023.
 CC XX
 CC Human; single exon probe; asthma; lung cancer; COPD; ILD;
 CC KW chronic obstructive pulmonary disease; interstitial lung disease;
 CC KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 CC KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
 CC KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 CC KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 CC KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 CC KW primary ciliary dyskinesia; pulmonary hypertension;
 CC KW hyaline membrane disease.
 CC XX
 CC OS Homo sapiens.
 CC XX
 CC EN WO200186003-A2.
 CC XX
 CC PD 15-NOV-2001.
 CC XX
 CC PF 30-JAN-2001; 2001WO-US000665.
 CC XX
 CC PR 04-FEB-2000; 2000US-0180312P.
 CC PR 26-MAY-2000; 2000US-0207456P.
 CC PR 30-JUN-2000; 2000US-00608408.
 CC PR 03-AUG-2000; 2000US-00632366.
 CC PR 21-SEP-2000; 2000US-0234687P.
 CC PR 27-SEP-2000; 2000US-0236359P.
 CC PR 04-OCT-2000; 2000GB-00024263.
 CC XX
 CC PA (MOLE-) MOLECULAR DYNAMICS INC.
 CC XX
 CC FI Penn SG, Hanzel DK, Chen W, Rank DR;
 CC XX
 CC DR WPI; 2002-114183/15.
 CC XX
 CC PT Spatially-addressable set of single exon nucleic acid probes, used to
 CC measure gene expression in human lung samples.
 CC XX
 CC PS Claim 27; SEQ ID NO 26023; 634pp; English.
 CC XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression to a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 CC XX Sequence 199 AA;
 CC
 CC Query Match 100.0%; Score 40; DB 5; Length 199;
 CC Best Local Similarity 100.0%; Pred. No. 5;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 NMVPPPR 7
 CC Db 34 NMVPPPR 40
 CC
 CC RESULT 19
 CC ABB04618
 CC ID ABB04618 standard; protein; 207 AA.
 CC XX
 CC AC ABB04618;
 CC XX
 CC DT 04-MAR-2002 (first entry)
 CC XX
 CC DE Human tubulin-like protein 23 SEQ ID NO:2.
 CC XX
 CC KW Human; tubulin-like protein 23; TLP23; malignant tumour;
 CC KW immunological disease; confused embryonic development.
 CC XX
 CC OS Homo sapiens.
 CC XX
 CC FN CN1306998-A.
 CC XX
 CC PD 08-AUG-2001.
 CC XX
 CC PF 31-JAN-2000; 2000CN-00111637.
 CC XX
 CC PR 31-JAN-2000; 2000CN-00111637.
 CC XX
 CC PA (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
 CC XX
 CC FI Mao Y, Xie Y;
 CC XX WPI; 2002-026879/04.
 CC DR N-PSDB; ABA04254.

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XX  New tubulin-like protein 23 polypeptide for treating malignant tumor,
PT  immunological diseases, and confused embryonic development.
XX
XX  Claim 1; Page 21-22 (Disclosure); 28pp; Chinese.
XX
XX  The present sequence represents human tubulin-like protein 23 (TLP23).
CC  The present invention also describes a method of applying TLP23 in the
CC  treatment of various diseases, such as malignant tumour, immunological
CC  diseases and confused embryonic development. The present invention also
CC  describes the antagonist resisting the polypeptide and its treatment
CC  effect
XX
XX  Sequence 207 AA;
SQ
    Query Match      100.0%; Score 40; DB 5; Length 207;
    Best Local Similarity 100.0%; Pred. No. 5.2;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 NMVPPFR 7
    Db  184 NMVPPFR 190
        |||||
        |||||

RESULT 20
ADD31371
ID  ADD31371 standard; protein; 209 AA.
XX
XX  ADD31371;
AC
XX
XX  15-JAN-2004 (first entry)
DT
XX
XX  White rot fungus beta-tubulin #SEQ ID 2.
DE
XX
XX  Pretreating; wood; white rot fungus; whitening; paper; T24li.
KW
XX
XX  Physisporinus rivulosus; T24li.
OS
XX
XX  WO2003080812-A1.
FN
XX
XX  02-OCT-2003.
PD
XX
XX  27-MAR-2003; 2003WO-FI000238.
PF
XX
XX  27-MAR-2002; 2002FI-00000591.
PR
XX
XX  (UYHE-) UNIV HELSINKI.
PA
XX
XX  Hatakka A, Maijala P, Hakala T, Hauhio L, Ellmen J;
PI
XX
XX  WPI; 2003-865120/80.
DR
XX
XX  Pretreating wood useful for paper making, involves inoculating white rot
PT  fungus Physisporinus rivulosus, into wood.
XX
XX  Example 15; SEQ ID NO 2; 45pp; English.
FS
XX
XX  The invention relates to a method for pretreating wood, involving
CC  inoculating white rot fungus Physisporinus rivulosus into wood. The white
CC  rot fungus is preferably Physisporinus rivulosus strain T24li. The method
CC  of the invention is useful for pretreatment of wood and whitening of its
CC  colour. The method is also useful for paper making. The current sequence
CC  represents the beta-tubulin-encoding protein from strain T24li.
XX
XX  Sequence 209 AA;
SQ
    Query Match      100.0%; Score 40; DB 7; Length 209;
    Best Local Similarity 100.0%; Pred. No. 5.3;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 NMVPPFR 7
    Db  57 NMVPPFR 63
        |||||
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RESULT 21
AAR21831
ID  AAR21831 standard; protein; 226 AA.
XX
XX  AAR21831;
AC
XX
XX  25-MAR-2003 (revised)
DT  23-JUL-1992 (first entry)
XX
XX  Sequence encoded by beta-tubulin gene.
DE
XX
XX  Worm infection; diagnosis; PCR primer; alpha-tubulin; beta-tubulin.
KW
XX
XX  Haemonchus contortus.
OS
XX
XX  WO9203549-A.
PN
XX
XX  05-MAR-1992.
PD
XX
XX  15-AUG-1991; 91WO-N0000153.
PF
XX
XX  16-AUG-1990; 90NL-00001832.
PR
XX
XX  (EUDI-) EURO-DIAGNOSTICS BV.
PA
XX
XX  Roos MH;
PI
XX
XX  WPI; 1992-096893/12.
DR  N-PSDB; AAQ22665.
XX
XX  DNA sequence used for diagnosing nematode infection - comprises alpha-
PT  and/or beta-tubulin gene of Haemonchus contortus.
XX
XX  Claim 15; Fig 2; 22pp; English.
XX
XX  The inventors claim a DNA sequence of a tubulin gene of Haemonchus
CC  contortus and a peptide comprising at least part of the the AA sequence
CC  encoded by it. Primers used in the diagnosis of worm infection corresp.
CC  to at least a conserved part of the tubulin gene, pref. the 3' half of (1
CC  -beta), located so that the amplification prod. has a species specific
CC  length per nematode. Two beta-tubulin oligonucleotides, beta-1 and beta-
CC  2, were made based on (1-beta) of H.C. in order to measure the difference
CC  in introns among various nematode species. Primers beta-7 and beta-8 take
CC  into account the degeneracy of the genetic code. (Updated on 25-MAR-2003
CC  to correct Pf field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX  Sequence 226 AA;
SQ
    Query Match      100.0%; Score 40; DB 2; Length 226;
    Best Local Similarity 100.0%; Pred. No. 5.7;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 NMVPPFR 7
    Db  34 NMVPPFR 40
        |||||
        |||||

RESULT 22
ADR09220
ID  ADR09220 standard; protein; 304 AA.
XX
XX  ADR09220;
AC
XX
XX  04-NOV-2004 (first entry)
DT
XX
XX  Human protein useful for treating neurological disease Seq 2726.
DE
XX
XX  human; oligo-capping method; diagnostic marker; gene therapy;
KW  osteoporosis; neurological disease; Alzheimer's disease;
KW  Parkinson's disease; dementia; short memory; cancer;
KW  sense or motor function; emotional reaction; fear response; panic;

```

KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW tranquilliser.
 XX
 OS Homo sapiens.
 XX
 PN EP1447413-A2.
 XX
 XX 18-AUG-2004.
 PD
 XX
 PF 12-FEB-2004; 2004EP-00003145.
 XX
 XX 14-FEB-2003; 2003JP-00102207.
 PR 09-MAY-2003; 2003JP-00131452.
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA
 XX Isoqai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;
 PI
 XX WPI; 2004-583265/57.
 DR N-PSDB; ADR07264.
 DR
 XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 PT
 XX Claim 1; SEQ ID NO 2726; 2686pp; English.
 PS
 XX This invention relates to novel, isolated full length human cDNA
 CC molecules and the encoded proteins thereof. Specifically, it refers to
 CC cDNA clones obtained by an oligo-capping method, where none of these
 CC clones are identical to any known human mRNAs. The present invention
 CC describes an immunoassay to identify agonists and antagonists, as well as
 CC antibodies, antisense molecules and siRNAs that can all be used to bind
 CC to and modulate expression of the cDNA molecules. As such, these
 CC molecules are useful for diagnostic markers or therapeutic targets for
 CC the various diseases or morbid states. In particular, they are useful in
 CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
 CC disease, Parkinson's disease, dementia, short memory and various cancers,
 CC as well as for maintaining equilibrium of sense or motor function, and
 CC for treating emotional reaction, fear response and panic. Accordingly,
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
 CC cytostatic and tranquilliser activities. This polypeptide is a protein
 CC encoded by a full length human cDNA sequence of the invention. NOTE: This
 CC sequence is not given in the sequence listing of the specification but
 CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
 CC office.
 XX
 SQ Sequence 304 AA;
 Query Match 100.0%; Score 40; DB 8; Length 304;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NMVPPPR 7
 Db 110 NMVPPPR 116
 RESULT 23
 ABG09486
 ID ABG09486 standard; protein; 328 AA.
 XX
 AC ABG09486;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #9477.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 XX Homo sapiens.
 OS
 XX

PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 XX 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS73673.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PT
 XX Claim 20; SEQ ID NO 39845; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: the sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 328 AA;
 Query Match 100.0%; Score 40; DB 4; Length 328;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NMVPPPR 7
 Db 149 NMVPPPR 155
 RESULT 24
 AAU21640
 ID AAU21640 standard; protein; 332 AA.
 XX
 AC AAU21640;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Novel human neoplastic disease associated polypeptide #73.
 XX
 XX Human; neoplastic disease associated polypeptide; cancer;
 KW hyperproliferative disorder; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW neuroprotective; cytostatic; anti inflammatory; vasotropic.
 XX
 OS Homo sapiens.
 XX

PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465558/50.
DR N-PSDB; AAS34839.
XX
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, and for treating cancers, rheumatoid arthritis.
XX
XX Claim 11; SEQ ID NO 367; 697pp; English.
XX
XX The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA
CC sequences encoding for these polypeptides. The sequences of the invention
CC are useful in the diagnosis, treatment, prevention and/or prognosis of
CC disorders involving neoplastic disease such as hyperproliferative
CC disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
CC glioma, adult liver cancer, childhood cerebellar astrocytoma, or
CC Hodgkin's lymphoma). The sequences of the invention may also be useful
CC for treating other disorders such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, pulmonary disorders, cardiovascular disorders and renal
CC disorders. The polynucleotide sequences of the invention are also useful
CC in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic
CC disease associated polypeptides of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 332 AA;
SQ

Query Match 100.0%; Score 40; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7
D5 142 NMVPPPR 148

RESULT 25
ADC46281
ID ADC46281 standard; protein; 332 AA.
XX
XX AC ADC46281;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human neoplastic disease-associated gene 73 protein #1.
XX
XX KW Neoplastic disease-associated polypeptide; gene therapy; diabetes;
KW hyperproliferative disease; cancer; autoimmune disorder;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;
KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; renal disorder;
KW acute glomerulonephritis; end-stage renal disease;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; AIDS; cachexia; anorexia; wound healing;
KW epithelial cell proliferation; Human.
XX
XX OS Homo sapiens.
XX
XX PN US2003082758-A1.
XX
XX PD 01-MAY-2003.
XX
XX PF 22-MAR-2002; 2002US-00103313.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR

24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0205535P.
07-JUN-2000; 2000US-0209467P.
28-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217496P.
14-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0220963P.
26-JUL-2000; 2000US-0220964P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0225213P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225267P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-0225270P.
14-AUG-2000; 2000US-0225447P.
14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225759P.
18-AUG-2000; 2000US-0226279P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226868P.
22-AUG-2000; 2000US-0227182P.
23-AUG-2000; 2000US-0227009P.
30-AUG-2000; 2000US-0228924P.
01-SEP-2000; 2000US-0229287P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
05-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0230437P.
06-SEP-2000; 2000US-0230438P.
08-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0232080P.
08-SEP-2000; 2000US-0232081P.
12-SEP-2000; 2000US-0231968P.
14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232398P.
14-SEP-2000; 2000US-0232399P.
14-SEP-2000; 2000US-0232400P.
14-SEP-2000; 2000US-0232401P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233064P.
21-SEP-2000; 2000US-0234223P.
21-SEP-2000; 2000US-0234274P.
25-SEP-2000; 2000US-0234997P.
25-SEP-2000; 2000US-0234998P.
26-SEP-2000; 2000US-0235484P.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246603P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 17-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2000US-0254097P.
PR 17-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764854.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-786918/74.
DR N-PSDB; ADC45997.
XX New isolated human neoplastic disease-associated polypeptides and
PT polynucleotides, useful for diagnosing, preventing, prognosticating or
PT treating medical conditions such as cancer, AIDS, diabetes or Parkinson's

PT disease.
XX Claim 11; SEQ ID NO 367; 302pp; English.
XX The invention relates to one of 238 disclosed human neoplastic disease-
CC associated polypeptides encoded by 171 disclosed cDNA sequences
CC (including their domains, epitopes, full-length proteins, allelic variants
CC or species homologues). Also included are there encoding nucleic acids, a
CC recombinant vector comprising the nucleic acid, a recombinant host cell
CC comprising the nucleic acid (expressing the protein), an isolated
CC antibody that binds specifically to the isolated polypeptide, preventing,
CC treating or ameliorating a medical condition, diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject,
CC identifying a binding partner to the polypeptide, identifying an activity
CC in a biological assay, and the gene corresponding to the cDNA sequence.
CC The polypeptides, polynucleotides and antibodies are useful for
CC detecting, preventing, diagnosing, prognosticating, treating or
CC ameliorating medical conditions such as hyperproliferative diseases or
CC cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
CC systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
CC or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
CC anaemia or thrombocytopaenia), allergic reactions including asthma or
CC eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,

Query Match 100.0%; Score 40; DB 7; Length 332;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NMVPPFR 7
Db 142 NMVPPFR 148
|||||

RESULT 26
AAMI3601
ID AAMI3601 standard; protein; 351 AA.
XX AAMI3601;
XX 12-OCT-2001 (first entry)
XX Peptide #35 encoded by probe for measuring cervical gene expression.
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer.
XX Homo sapiens.
XX WO200157278-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000670.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.
XX Claim 27; SEQ ID NO 18427; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes
 CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 351 AA;

Query Match 100.0%; Score 40; DB 4; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7
 Db 163 NMVPPPR 169

RESULT 27

ABB2530
 ID ABB2530 standard; peptide; 351 AA.

XX AC ABB2530;

XX DT 01-FEB-2002 (first entry)

XX DE Peptide #36 encoded by human foetal liver single exon nucleic acid probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX FN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human foetal liver.

XX Claim 27; SEQ ID NO 25165; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
 XX human gene expression in a sample derived from human foetal liver. The
 XX single exon nucleic acid probes may be used for predicting, measuring and
 XX displaying gene expression in samples derived from human foetal liver. The
 XX present sequence is a peptide encoded by a single exon nucleic acid probe
 XX of the invention. Note: The sequence data for this patent did not form
 XX part of the printed specification, but was obtained in electronic format
 XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 351 AA;

Query Match 100.0%; Score 40; DB 4; Length 351;

Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7
 Db 163 NMVPPPR 169

RESULT 28

AAM25998
 ID AAM25998 standard; protein; 351 AA.

XX AC AAM25998;

XX DT 17-OCT-2001 (first entry)

XX DE Peptide #35 encoded by probe for measuring placental gene expression.

XX KW Probe; microarray; human; placenta; antenatal diagnosis;
 XX genetic disorder.

XX OS Homo sapiens.

XX FN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 27; SEQ ID NO 26267; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:
 XX see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 XX such probe. The probes are useful for producing a microarray for
 XX predicting, measuring and displaying gene expression in samples derived
 XX from human placenta. The probes are useful for antenatal diagnosis of
 XX human genetic disorders

XX Sequence 351 AA;

Query Match 100.0%; Score 40; DB 4; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7
 Db 163 NMVPPPR 169

RESULT 29

ABB27382
 ID ABB27382 standard; peptide; 351 AA.

XX AC ABB27382;

XX DT 01-FEB-2002 (first entry)

XX DE Human peptide #33 encoded by breast cell single exon nucleic acid probe.
 XX KW Human; microarray; single exon probe; gene expression; breast; disease;
 XX KW cancer.
 XX OS Homo sapiens.
 XX PN WO200157271-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000662.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-496933/54.
 XX DR New spatially-addressable set of single exon nucleic acid probes, useful
 XX PT for measuring gene expression in sample derived from human breast,
 XX PT comprises number of single exon nucleic acid probes.
 XX PS Claim 27; SEQ ID NO 10350; 327pp + Sequence Listing; English.
 XX CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BR 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 351 AA;
 Query Match 100.0%; Score 40; DB 4; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMVPPFR 7
 Db 163 NMVPPFR 169
 RESULT 30
 ABB18034
 ID ABB18034 standard; protein; 351 AA.
 XX AC ABB18034;
 XX DT 23-JAN-2002 (first entry)
 XX DE Protein #33 encoded by probe for measuring heart cell gene expression.

XX KW Human; gene expression; heart; microarray; vascular system;
 XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
 XX KW congenital heart disease.
 XX OS Homo sapiens.
 XX PN WO200157274-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000666.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX DR Single exon nucleic acid probes for analyzing gene expression in human
 XX PT hearts.
 XX PS Claim 15; SEQ ID NO 19804; 530pp; English.
 XX CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 351 AA;
 Query Match 100.0%; Score 40; DB 4; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMVPPFR 7
 Db 163 NMVPPFR 169
 RESULT 31
 AAM65742
 ID AAM65742 standard; protein; 351 AA.
 XX AC AAM65742;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26048.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX OS Homo sapiens.
 XX PN WO200157276-A2.

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PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 26048; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
SQ Sequence 351 AA;
Query Match 100.0%; Score 40; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NMVPFPR 7
Db 163 NMVPFPR 169
RESULT 32
AAM53363
ID AAM53363 standard; protein; 351 AA.
XX
AC AAM53363;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25468.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

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XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 25468; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
SQ Sequence 351 AA;
Query Match 100.0%; Score 40; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NMVPFPR 7
Db 163 NMVPFPR 169
RESULT 33
ABG47383
ID ABG47383 standard; peptide; 351 AA.
XX
AC ABG47383;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID NO 26031.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 26031; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression

```

CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 351 AA;

Query Match 100.0%; Score 40; DB 4; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Indels 0; Gaps 0;

Qy 1 NMVFPFR 7
 |||||
 Db 163 NMVFPFR 169

RESULT 34
 ID AAM01351 standard; protein; 351 AA.

XX AC AAM01351;

XX DT 09-OCT-2001 (first entry)

XX DE Peptide #33 encoded by probe for measuring human breast gene expression.

XX KW Probe; human; breast disease; breast cancer; development disorder;
 XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX OS Homo sapiens.

XX PN WO200157270-A2.

XX PD 09-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US000661.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX FI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-476286/51.

XX PT Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.

XX PS Claim 27; SEQ ID NO 10091; 322pp; English.

XX CC The present invention relates to novel single exon nucleic acid probes
 CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer; disorders of development,
 CC inflammatory diseases of the breast; fibrocystic changes; proliferative
 CC breast disease and non-carcinoma tumours. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 351 AA;

Query Match 100.0%; Score 40; DB 4; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Indels 0; Gaps 0;

Qy 1 NMVFPFR 7
 |||||
 Db 163 NMVFPFR 169

RESULT 35
 ID ABG35371 standard; peptide; 351 AA.

XX AC ABG35371;

XX DT 19-AUG-2002 (first entry)

XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 25036.

XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.

XX OS Homo sapiens.

XX PN WO200186003-A2.

XX PD 15-NOV-2001.

XX PF 30-JAN-2001; 2001WO-US000665.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX FI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2002-114183/15.

XX PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.

XX PS Claim 27; SEQ ID NO 25036; 634pp; English.

XX CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Kargener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at fcp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 351 AA;

Query Match 100.0%; Score 40; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
 |||||
 Db 163 NMVPPPR 169

RESULT 36
 AAB08516
 ID AAB08516 standard; peptide; 352 AA.

AC AAB08516;

DT 20-DEC-2000 (first entry)

DE Amino acid sequence of a beta-tubulin antigen.

KW Beta-tubulin antigen; inner ear protein; Meniere's disease; autoantibody;
 KW chronic ear disease; autoimmune disease.

OS Homo sapiens.

PN WO200050593-A1.

PD 31-AUG-2000.

PF 25-FEB-2000; 2000WO-US004795.

PR 25-FEB-1999; 99US-0121549P.

PA (UYTE-) UNIV TENNESSEE RES CORP.

PI Yoo TJ;

DR WPI; 2000-558400/51.

PT New beta-tubulin antigen in the membranous structure of the inner ear,
 PT reactive with antibodies of patients with Meniere's disease, for
 PT diagnosing Meniere's disease and distinguishing this disease from other
 PT autoimmune ear diseases.

PS Claim 3; Page 47-48; 115pp; English.

CC The present sequence represents a beta-tubulin antigen. It is encoded by

CC an exon of AAA64133, and is a fragment of the protein given in AAB08430.
 CC The protein is an antigen of the membranous structure of the inner ear
 CC protein, and is reactive with antibodies from patients having Meniere's
 CC disease. Meniere's disease is a chronic ear disease with unknown
 CC etiology. Serum from patients suffering from this disease contain
 CC autoantibodies against a 30 kDa cochlear protein antigen. The disease is
 CC believed to be an autoimmune disease. The beta-tubulin antigen is useful
 CC as a target substance in diagnosing or detecting Meniere's disease and in
 CC distinguishing this disease from other autoimmune ear diseases

SQ Sequence 352 AA;

Query Match 100.0%; Score 40; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
 |||||
 Db 164 NMVPPPR 170

RESULT 37

ADS23336
 ID ADS23336 standard; protein; 355 AA.

XX ADS23336;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #12369.

KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

OS Bacteria.

PN US2003233675-A1.

PD 18-DEC-2003.

PF 20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

PS Claim 1; SEQ ID NO 12369; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the

recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 355 AA;

Query Match 100.0%; Score 40; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| | | | |
Db 139 NMVPPFR 145

RESULT 38
AD7F4154
ID AD7F4154 standard; protein; 370 AA.

XX AC AD7F4154;

XX DT 26-FEB-2004 (first entry)

XX DE Human novel brain/hippocampus protein #42.

XX KW Human, brain; hippocampus; gene therapy; mental illness;
proteome analysis.

XX OS Homo sapiens.

XX PN JP2003009886-A.

XX PD 14-JAN-2003.

XX PF 21-DEC-2001; 2001JP-00390441.

XX PR 22-DEC-2000; 2000JP-00389742.

XX PR 29-MAR-2001; 2001JP-00095524.

XX PR 25-APR-2001; 2001JP-00127066.

XX PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX PA (PROT-) PROTEIN EXPRESS KK.

XX DR WPI; 2003-735084/70.

XX DR N-ESDB; ADF74224.

XX FS Claim 1; SEQ ID NO 42; 319pp; Japanese.

XX CC The invention relates to an isolated human polypeptide consisting of a sequence of any one of 70 fully defined sequences (S1) appearing as ADF74113-ADF74182 being encoded by one of 70 disclosed cDNA sequences isolated from brain or hippocampus tissue, or a sequence of (S1) having deletion, substitution, or addition and essentially retaining the same biological activity of (S1). Also included are DNA that encodes the protein, DNA which hybridises with the encoding DNA and codes a polypeptide which substantially as the same activity as that of a polypeptide above, a gene including the DNA, a recombinant polypeptide

CC encoded by the gene, an antibody against the protein, DNA chip which comprises the DNA, a polypeptide chip comprising the protein, an antibody chip comprising the antibody, a recombinant vector containing the DNA, a transformed host cell containing the vector, an antisense polynucleotide which has a sequence complementary to the DNA, a kit for screening compounds that interact with the protein, test compounds which interact with the protein and homologous proteins having 70% sequence identity with (S1). The protein is useful for identifying compounds which interact with the protein e.g., compounds which inhibit or activate the protein. Compounds that inhibit the protein activity are useful as therapeutic agents for treating disorders characterised by aberrant protein activity. The DNA is useful for producing the protein by recombinant techniques, as a probe in diagnostic techniques for detecting abnormalities in the gene, and in gene therapy techniques. The DNA is useful for creating animal models of disease. The DNA chips are useful for diagnosing any abnormalities of the DNA in biological samples obtained from human subjects, where the abnormalities result in mental illness. The protein is useful for detecting the protein in biological samples. The protein chip is useful for functional analysis of the protein, e.g. expression of the protein, interaction of the protein, post-translational modification of the protein. The antibody chip is useful for analysing disease states associated with polypeptide. The antibody chip is also useful in proteome analysis. The present sequence represents a human brain/hippocampus protein of the invention.

XX SQ Sequence 370 AA;

Query Match 100.0%; Score 40; DB 7; Length 370;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| | | | |
Db 180 NMVPPFR 186

RESULT 39

ADE15634
ID ADE15634 standard; protein; 374 AA.

XX AC ADE15634;

XX DT 29-JAN-2004 (first entry)

XX DE Human structural and cytoskeleton-associated protein (SCAP) #13.

XX KW human; structural and cytoskeleton-associated protein; SCAP;
arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; myelofibrosis;
psoriasis; cancer; pneumonia; chronic bronchitis; yellow fever;
influenza; measles; mumps; HIV; human T lymphotropic virus; rabies;
gastroenteritis; encephalitis; rubella; epilepsy;
XW ischaemic cerebrovascular disease; stroke; cerebral neoplasm;
XW Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
XW Parkinson's disease; amyotrophic lateral sclerosis; atrophy;
XW hereditary ataxia; multiple sclerosis; meningitis; brain abscess;
XW prion disease; Creutzfeldt-Jakob disease; insomnia; neurofibromatosis;
XW cerebral palsy; myasthenia gravis; anxiety.

XX OS Homo sapiens.

XX PN WO2003062391-A2.

XX PD 31-JUL-2003.

XX PF 16-JAN-2003; 2003WO-US001772.

XX PR 18-JAN-2002; 2002US-0350702P.

XX PR 25-JAN-2002; 2002US-0351715P.

XX PR 15-FEB-2002; 2002US-0357402P.

XX PR 10-MAY-2002; 2002US-0379880P.

XX PR 17-MAY-2002; 2002US-0381599P.

XX PR 07-JUN-2002; 2002US-0387270P.

XX PR 19-JUL-2002; 2002US-0397125P.


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XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Yue H, Griffin JA, Richardson TW, Tang YT, Thangavelu K;
XX PI Foreythe IJ, Becha SD, Chawla NK, Hafalia AJA, Swarnakar A;
XX PI Marquis JP, Gorvad AE, Baughn MR, Lu DAM, Arvizu CS, Kable AE;
XX PI Lee SY, Ramkumar J, Jiang X, Jackson AA, Khare R, Elliott VS;
XX PI Bulloch SA, Xu Y, Lee S, Lehr-Mason PM;
XX DR WPI; 2003-671468/63.
XX DR N-PSDB; ADE15665.
XX PT New isolated polypeptides useful for treating e.g. cell proliferative
XX PT disorders, viral infections and neurological disorders.
XX PS Claim 1; SEQ ID NO 13; 357pp; English.
XX CC The invention comprises the amino acid and coding sequences of human
XX CC structural and cytoskeleton-associated proteins (SCAP). The SCAP DNA and
XX CC protein sequences of the invention are useful for the diagnosis and
XX CC treatment of: arteriosclerosis, atherosclerosis, cirrhosis, hepatitis,
XX CC myelofibrosis, psoriasis, primary cancer, pneumonia, chronic bronchitis,
XX CC yellow fever, influenza, measles, mumps, HIV, human T lymphotropic virus,
XX CC rabies, gastroenteritis, encephalitis, rubella, epilepsy, ischaemic
XX CC cerebrovascular disease, stroke, cerebral neoplasm, Alzheimer's disease,
XX CC Pick's disease, Huntington's disease, dementia, Parkinson's disease,
XX CC amyotrophic lateral sclerosis, atrophy, hereditary ataxias, multiple
XX CC sclerosis, meningitis, brain abscess, prion disease, Creutzfeldt-Jakob
XX CC disease, insomnia, neurofibromatosis, cerebral palsy, myasthenia gravis,
XX CC anxiety. The present amino acid sequence represents a human SCAP of the
XX CC invention.
XX SQ Sequence 374 AA;
    Query Match 100.0%; Score 40; DB 7; Length 374;
    Best Local Similarity 100.0%; Pred. No. 9.5;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NMVPPFR 7
Db 185 NMVPPFR 191
    |||||
    |||||

RESULT 40
AAB93707
ID AAB93707 standard; protein; 397 AA.
XX AC AAB93707;
XX DT 26-JUN-2001 (first entry)
XX DE Human protein sequence SEQ ID NO:13297.
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX OS Homo sapiens.
XX PN EP1074617-A2.
XX PD 07-FEB-2001.
XX PF 28-JUL-2000; 2000EP-00116126.
XX PR 29-JUL-1999; 99JP-00248036.
XX PR 27-AUG-1999; 99JP-00300253.
XX PR 11-JAN-2000; 2000JP-00118776.
XX PR 02-MAY-2000; 2000JP-00183767.
XX PR 09-JUN-2000; 2000JP-00241899.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

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XX WPI; 2001-318749/34.
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX PT length cDNAs defined in the specification, and for the detection and/or
XX PT diagnosis of the abnormality of the proteins encoded by the full-length
XX PT cDNAs.
XX PS Claim 8; SEQ ID NO 13297; 2537pp + Sequence Listing; English.
XX CC The present invention describes primer sets for synthesising 5602 full-
XX CC length cDNAs defined in the specification. Where a primer set comprises:
XX CC (a) an oligo-dT primer and an oligonucleotide complementary to the
XX CC complementary strand of a polynucleotide which comprises one of the 5602
XX CC nucleotide sequences defined in the specification, where the
XX CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX CC of an oligonucleotide comprising a sequence complementary to the
XX CC complementary strand of a polynucleotide which comprises a 5'-end
XX CC sequence and an oligonucleotide comprising a sequence complementary to a
XX CC polynucleotide which comprises a 3'-end sequence, where the
XX CC oligonucleotide comprises at least 15 nucleotides and the combination of
XX CC the 5'-end sequence/3'-end sequence is selected from those defined in the
XX CC specification. The primer sets can be used in antisense therapy and in
XX CC gene therapy. The primers are useful for synthesising polynucleotides,
XX CC particularly full-length cDNAs. The primers are also useful for the
XX CC detection and/or diagnosis of the abnormality of the proteins encoded by
XX CC the full-length cDNAs. The primers allow obtaining of the full-length
XX CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX CC AAH13633 to AAH18742 represent human cDNA sequences; AA892446 to AA895893
XX CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX CC oligonucleotides, all of which are used in the exemplification of the
XX CC present invention.
XX SQ Sequence 397 AA;
    Query Match 100.0%; Score 40; DB 4; Length 397;
    Best Local Similarity 100.0%; Pred. No. 10;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NMVPPFR 7
Db 208 NMVPPFR 214
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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	40	100.0	445	2	US-08-935-450-4
2	40	100.0	445	4	US-09-338-123-4
3	37	92.5	319	4	US-09-248-796A-20600
4	37	92.5	449	4	US-09-202-329-8
5	34	85.0	200	3	US-09-183-861-84
6	34	85.0	200	3	US-09-022-765-84
7	34	85.0	200	4	US-09-551-974A-84
8	34	85.0	200	4	US-09-565-501A-108
9	34	85.0	200	4	US-09-639-206A-108
10	34	85.0	200	4	US-09-874-923-84
11	34	85.0	429	4	US-09-902-540-15942
12	34	85.0	448	4	US-09-792-024-101
13	34	85.0	451	4	US-09-565-501A-108
14	34	85.0	451	4	US-09-639-206A-108
15	34	85.0	451	4	US-09-874-923-108
16	34	85.0	455	4	US-09-949-016-8345
17	34	85.0	471	4	US-09-949-016-8344
18	34	85.0	473	4	US-09-949-016-7447
19	34	85.0	475	4	US-09-270-767-41691
20	32	80.0	2254	2	US-08-677-010-3
21	32	80.0	2254	2	US-08-790-519-3
22	31	77.5	168	4	US-09-134-000C-3463
23	31	77.5	195	4	US-09-107-532A-3908
24	31	77.5	199	4	US-09-248-796A-20525
25	30	75.0	34	1	US-08-441-534A-14
26	30	75.0	34	1	US-08-629-752-14
27	30	75.0	34	2	US-08-802-991-14

28	30	75.0	84	4	US-09-248-796A-19155	Sequence 19155, A
29	30	75.0	110	4	US-09-270-767-48123	Sequence 48123, A
30	30	75.0	227	1	US-08-360-103A-2	Sequence 2, Appli
31	30	75.0	475	4	US-09-543-681A-7150	Sequence 7150, Ap
32	30	75.0	487	4	US-09-489-039A-12031	Sequence 12031, A
33	30	75.0	532	3	US-08-911-321-11	Sequence 11, Appl
34	30	75.0	550	4	US-09-489-039A-7879	Sequence 7879, Ap
35	30	75.0	803	4	US-09-252-991A-28469	Sequence 28469, A
36	30	75.0	1328	3	US-08-781-891-76	Sequence 76, Appl
37	30	75.0	1328	4	US-09-618-166-76	Sequence 76, Appl
38	29	72.5	61	4	US-09-107-532A-5451	Sequence 5451, Ap
39	29	72.5	65	4	US-09-248-796A-22273	Sequence 22273, A
40	29	72.5	97	4	US-09-673-395A-388	Sequence 388, App
41	29	72.5	100	4	US-09-902-540-16481	Sequence 16481, A
42	29	72.5	111	4	US-09-513-999C-8085	Sequence 8085, Ap
43	29	72.5	116	4	US-09-252-991A-19096	Sequence 19096, A
44	29	72.5	138	4	US-09-198-452A-471	Sequence 471, App
45	29	72.5	153	4	US-10-141-225-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-935-450-4
; Sequence 4, Application US/08935450
; Patent No. 5977311
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, MeiJia
; APPLICANT: Schulz, Vincent
; TITLE OF INVENTION: 53BP2 COMPLEXES
; FILE REFERENCE: 7934-054
; CURRENT APPLICATION NUMBER: US/08/935,450
; CURRENT FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-935-450-4

Query Match 100.0%; Score 40; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 256 NMVPFPR 262

RESULT 2
US-09-338-123-4
; Sequence 4, Application US/09338123
; Patent No. 6627405
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, MeiJia
; APPLICANT: Schulz, Vincent
; TITLE OF INVENTION: 53BP2 COMPLEXES
; FILE REFERENCE: 7934-054
; CURRENT APPLICATION NUMBER: US/09/338,123
; CURRENT FILING DATE: 1999-06-22
; EARLIER APPLICATION NUMBER: 08/935,450
; EARLIER FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-338-123-4

Query Match 100.0%; Score 40; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 6.8; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
|:|||||
Db 256 NLVPFPR 262

RESULT 3

US-09-248-796A-20600
; Sequence 20600, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20600
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20600

Query Match 92.5%; Score 37; DB 4; Length 319;
Best Local Similarity 85.7%; Pred. No. 18; 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
|:|||||
Db 126 NLVPFPR 132

RESULT 4

US-09-202-329-8
; Sequence 8, Application US/09202329A
; Patent No. 6676944
; GENERAL INFORMATION:
; APPLICANT: Dalton, John P
; TITLE OF INVENTION: Vaccine containing a peroxiredoxin and/or a B-tubulin
; FILE REFERENCE: 1181-243
; CURRENT APPLICATION NUMBER: US/09/202,329A
; CURRENT FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: GB 9612214.8
; EARLIER FILING DATE: 1996-06-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01573
; EARLIER FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
; PUBLICATION INFORMATION:
; AUTHORS: Nagel, S. D.
; AUTHORS: Boothroyd, J. C.
; TITLE: The a and b tubulins of Toxoplasma gondii are encoded
; TITLE: by single copy genes containing multiple copy introns.
; JOURNAL: Mol. Biochem. Parasitol.
; VOLUME: 29
; PAGES: 261-273
; DATE: 1988
; PUBLICATION INFORMATION:
; TITLE: GenBank Accession no. F10878

US-09-202-329-8

Query Match 92.5%; Score 37; DB 4; Length 449;
Best Local Similarity 85.7%; Pred. No. 25; 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
|:|||||
Db 256 NLVPFPR 262

RESULT 5

US-09-183-861-84
; Sequence 84, Application US/09183861
; Patent No. 6365165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/022,765
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-183-861-84

Query Match 85.0%; Score 34; DB 3; Length 200;
Best Local Similarity 71.4%; Pred. No. 41; 0; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
|:|||||
Db 7 NLVPFPR 13

RESULT 6

US-09-022-765-84
; Sequence 84, Application US/09022765
; Patent No. 6375955
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio

```

; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,765
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-09-022-765-84

Query Match 85.0%; Score 34; DB 3; Length 200;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 7 NLPVYPR 13

RESULT 7
US-09-551-974A-84
; Sequence 84, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-551-974A-84

Query Match 85.0%; Score 34; DB 4; Length 200;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 7 NLPVYPR 13

RESULT 8
US-09-565-501A-84
; Sequence 84, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565,501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-565-501A-84

Query Match 85.0%; Score 34; DB 4; Length 200;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 7 NLPVYPR 13

RESULT 9
US-09-639-206A-84
; Sequence 84, Application US/09639206A
; Patent No. 6613337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-639-206A-84

Query Match 85.0%; Score 34; DB 4; Length 200;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 7 NLPVYPR 13
```

RESULT 10
 US-09-874-923-84
 ; Sequence 84, Application US/09874923
 ; Patent No. 6638517
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Coler, Rhea
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Brannon, Mark
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; FILE REFERENCE: 210121.420C8
 ; CURRENT APPLICATION NUMBER: US/09/874,923
 ; CURRENT FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 84
 ; LENGTH: 200
 ; TYPE: PRT
 ; ORGANISM: Leishmania major
 ; ORGANISM: Leishmania major

Query Match 85.0%; Score 34; DB 4; Length 200;
 Best Local Similarity 71.4%; Pred. No. 41;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
 |::||
 Db 7 NLVPYPR 13

RESULT 11
 US-09-902-540-15942
 ; Sequence 15942, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 15942
 ; LENGTH: 429
 ; TYPE: PRT
 ; ORGANISM: Myxococcus xanthus
 ; ORGANISM: Myxococcus xanthus

Query Match 85.0%; Score 34; DB 4; Length 429;
 Best Local Similarity 85.7%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
 |::||
 Db 175 NAVPFPR 181

RESULT 12
 US-09-792-024-101
 ; Sequence 101, Application US/09792024
 ; Patent No. 6783985
 ; GENERAL INFORMATION:

; APPLICANT: Roemer, Terry
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Boone, Charles
 ; APPLICANT: Bussey, Howard
 ; TITLE OF INVENTION: Gene Disruption Methodologies for Drug
 ; TITLE OF INVENTION: Targets Discovery
 ; FILE REFERENCE: 10182-004-999
 ; CURRENT APPLICATION NUMBER: US/09/792,024
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 490
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 101
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 ; ORGANISM: Candida albicans
 ; ORGANISM: Candida albicans

Query Match 85.0%; Score 34; DB 4; Length 448;
 Best Local Similarity 71.4%; Pred. No. 90;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
 |::||
 Db 259 NLVPYPR 265

RESULT 13
 US-09-565-501A-108
 ; Sequence 108, Application US/09565501A
 ; Patent No. 6607731
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Coler, Rhea
 ; APPLICANT: Peter, Probst
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; FILE REFERENCE: 210121.420C6
 ; CURRENT APPLICATION NUMBER: US/09/565,501A
 ; CURRENT FILING DATE: 2000-05-05
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 108
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Leishmania major
 ; ORGANISM: Leishmania major

Query Match 85.0%; Score 34; DB 4; Length 451;
 Best Local Similarity 71.4%; Pred. No. 90;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
 |::||
 Db 258 NLVPYPR 264

RESULT 14
 US-09-639-206A-108
 ; Sequence 108, Application US/09639206A
 ; Patent No. 6613337
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Coler, Rhea

; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-639-206A-108

Query Match 85.0%; Score 34; DB 4; Length 451;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|:|:|:|
Db 258 NLVPYPR 264

RESULT 15

US-09-874-923-108

; Sequence 108, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, David C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-874-923-108

Query Match 85.0%; Score 34; DB 4; Length 451;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|:|:|:|
Db 258 NLVPYPR 264

RESULT 16

US-09-949-016-8345

; Sequence 8345, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; SOFTWARE: FastSeq for Windows Version 4.0

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8345
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8345

Query Match 85.0%; Score 34; DB 4; Length 455;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|:|:|:|
Db 262 NLVPYPR 268

RESULT 17

US-09-949-016-8344

; Sequence 8344, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8344
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8344

Query Match 85.0%; Score 34; DB 4; Length 471;
Best Local Similarity 71.4%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|:|:|:|
Db 278 NLVPYPR 284

RESULT 18

US-09-949-016-7447

; Sequence 7447, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 7447
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7447

Query Match      85.0%; Score 34; DB 4; Length 473;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NMVPFPR 7
      |:|:|:|
Db      282 NLVPYPR 288

RESULT 19
US-09-270-767-41691
; Sequence 41691, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41691
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41691

Query Match      85.0%; Score 34; DB 4; Length 475;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NMVPFPR 7
      |:|:|:|
Db      285 NLVPYPR 291

RESULT 20
US-08-677-010-3
; Sequence 3, Application US/08677010
; Patent No. 5925805
; GENERAL INFORMATION:
; APPLICANT: Ohlrogge, John B.
; APPLICANT: Roesler, Keith R.
; APPLICANT: Shorrosh, Basil S.
; TITLE OF INVENTION: Structure and Expression of an
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 6550-00002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2254 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-677-010-3

Query Match      80.0%; Score 32; DB 2; Length 2254;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 NMVPPFR 7
Db 1383 DLVPPFR 1389

RESULT 22
US-09-134-000C-3463
; Sequence 3463, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3463
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3463

Query Match 77.5%; Score 31; DB 4; Length 168;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 6
Db 33 NMIPVP 38

RESULT 23
US-09-107-532A-3908
; Sequence 3908, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3908:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 195 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...195
; SEQUENCE DESCRIPTION: SEQ ID NO: 3908:
US-09-107-532A-3908

Query Match 77.5%; Score 31; DB 4; Length 195;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 6
Db 32 NMIPVP 37

RESULT 24
US-09-248-796A-20525
; Sequence 20525, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20525
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20525

Query Match 77.5%; Score 31; DB 4; Length 199;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 73 DMVPPQ 79

RESULT 25
US-08-441-534A-14
; Sequence 14, Application US/08441534A
; Patent No. 5561054
; GENERAL INFORMATION:
; APPLICANT: Michael A. Kron and Reuben Leberman
; TITLE OF INVENTION: Recombinant Asparaginyl-
; TITLE OF INVENTION: tRNA Synthetase From The Human
; TITLE OF INVENTION: Filarial Parasite, Brugia malayi
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 kb
; MEDIUM TYPE: storage
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COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version 3.3)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441.534A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: Motif of Synthetase
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
IMMEDIATE SOURCE:
LIBRARY:
US-08-441-534A-14

Query Match 75.0%; Score 30; DB 1; Length 34;
Best Local Similarity 57.1%; Pred. No. 40;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPR 7
Db 28 DVIPPR 34

RESULT 26
US-08-629-752-14
Sequence 14, Application US/08629752
Patent No. 572116
GENERAL INFORMATION:
APPLICANT: Michael A. Kron and Reuben Leberman
TITLE OF INVENTION: Recombinant Asparaginyl-
TITLE OF INVENTION: tRNA Synthetase From The Human
TITLE OF INVENTION: Filarial Parasite, Bruglia malayi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 kb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (version 3.3)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629.752
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441.534
FILING DATE: May 15, 1995
ATTORNEY/AGENT INFORMATION:

COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version 3.3)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441.534A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: Motif of Synthetase
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
IMMEDIATE SOURCE:
LIBRARY:
US-08-629-752-14

Query Match 75.0%; Score 30; DB 1; Length 34;
Best Local Similarity 57.1%; Pred. No. 40;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPR 7
Db 28 DVIPPR 34

RESULT 27
US-08-802-991-14
Sequence 14, Application US/08802991
Patent No. 5846771
GENERAL INFORMATION:
APPLICANT: Michael A. Kron and Reuben Leberman
TITLE OF INVENTION: Recombinant Asparaginyl-
TITLE OF INVENTION: tRNA Synthetase From The Human
TITLE OF INVENTION: Filarial Parasite, Bruglia malayi
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 kb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (version 3.3)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802.991
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/628.103
FILING DATE: April 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-358
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
```

; TOPOLOGY: Linear
 ; MOLECULE TYPE:
 ; DESCRIPTION: Motif of Synthetase
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Saccharomyces cerevisiae
 ; IMMEDIATE SOURCE:
 ; LIBRARY:
 US-08-802-991-14

Query Match 75.0%; Score 30; DB 2; Length 34;
 Best Local Similarity 57.1%; Pred. No. 40;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFP 7
 Db 28 DVIPFP 34

RESULT 28
 US-09-248-796A-19155
 ; Sequence 19155, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 19155
 ; LENGTH: 84
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-19155

Query Match 75.0%; Score 30; DB 4; Length 84;
 Best Local Similarity 66.7%; Pred. No. 97;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFP 6
 Db 21 NIIPFP 26

RESULT 29
 US-09-270-767-48123
 ; Sequence 48123, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 48123
 ; LENGTH: 110
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-48123

Query Match 75.0%; Score 30; DB 4; Length 110;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMVPFP 6
 Db 62 NMVPFP 67

RESULT 30
 US-08-360-103A-2
 ; Sequence 2, Application US/08360103A
 ; Patent No. 5674499
 ; GENERAL INFORMATION:
 ; APPLICANT: Willemse, Marja J.
 ; APPLICANT: Sondermeijer, Paul J.A.
 ; APPLICANT: Nicolson, Lesley
 ; TITLE OF INVENTION: Vaccine for the protection of horses
 ; TITLE OF INVENTION: against Equine herpesvirus infection.
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Organon Teknika Corporation
 ; STREET: 1330 Piccard Drive
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850-4377
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,103A
 ; FILING DATE: 20-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 93.203.584.3
 ; FILING DATE: 20-DEC-1993
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 227 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-360-103A-2

Query Match 75.0%; Score 30; DB 1; Length 227;
 Best Local Similarity 57.1%; Pred. No. 2.6e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFP 7
 Db 221 HIIPFP 227

RESULT 31
 US-09-543-681A-7150
 ; Sequence 7150, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 7150
 ; LENGTH: 475
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-7150

Query Match 75.0%; Score 30; DB 4; Length 475;
 Best Local Similarity 66.7%; Pred. No. 5.3e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPF 6
|:|:|
Db 2 NVIPFP 7

RESULT 32
US-09-489-039A-12031
; Sequence 12031, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12031
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12031

Query Match 75.0%; Score 30; DB 4; Length 487;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
:::|:|
Db 474 DVIPFPR 480

RESULT 33
US-08-911-321-11
; Sequence 11, Application US/08911321
; Patent No. 6010703
; GENERAL INFORMATION:
; APPLICANT: Roger K. Maes and Stephen J. Spatz
; TITLE OF INVENTION: Recombinant Poxvirus
; TITLE OF INVENTION: Vaccine Against
; TITLE OF INVENTION: Feline Rhinotracheitis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,183
; FILING DATE: July 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103

TELEX: No. 6010703e
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Polypeptide
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Feline herpesvirus-1
; STRAIN: 1
; INDIVIDUAL ISOLATE: C-27
; CELL TYPE: N/A
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD: Deduced Sequence
; OTHER INFORMATION: GB
US-08-911-321-11

Query Match 75.0%; Score 30; DB 3; Length 532;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPF 6
|:|:|
Db 432 NVIPFP 437

RESULT 34
US-09-489-039A-7879
; Sequence 7879, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7879
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7879

Query Match 75.0%; Score 30; DB 4; Length 550;
Best Local Similarity 71.4%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
|:|:|
Db 281 NAAPFPR 287

RESULT 35
US-09-252-991A-28469
; Sequence 28469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28469
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28469

Query Match 75.0%; Score 30; DB 4; Length 803;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MVPPFR 7
| : ||||
Db 9 MTPFR 14

RESULT 36
US-08-781-891-76
; Sequence 76, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-76

Query Match 75.0%; Score 30; DB 3; Length 1328;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| : ||||
Db 217 NNLPPFR 223

RESULT 37

US-09-618-166-76
; Sequence 76, Application US/09618166
; Patent No. 6583112
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/618,166
; FILING DATE: 17-Jul-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.419C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-618-166-76

Query Match 75.0%; Score 30; DB 4; Length 1328;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| : ||||
Db 217 NNLPPFR 223

RESULT 38
US-09-107-532A-5451
; Sequence 5451, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>

```
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5451:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...61
; SEQUENCE DESCRIPTION: SEQ ID NO: 5451:
US-09-107-532A-5451
```

```
Query Match 72.5%; Score 29; DB 4; Length 61;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 NMVPFPR 7
Db 28 NPVPFPQ 34
```

```
RESULT 39
US-09-248-796A-22273
; Sequence 22273, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22273
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22273
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Query Match 72.5%; Score 29; DB 4; Length 65;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 NMVPFPR 7
Db 56 NQPFPR 62
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RESULT 40
US-09-673-395A-388
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; Sequence 388, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 388
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-388
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Query Match 72.5%; Score 29; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 MVEFP 6
Db 93 MVEFP 97
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Search completed: July 20, 2005, 17:33:30
Job time : 16.5556 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 20, 2005, 17:31:44 ; Search time 56.5185 Seconds
(without alignments)
48.078 Million cell updates/sec

Title: US-10-766-480A-1

Perfect score: 40

Sequence: 1 NMVPPFR 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 388188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	10	10	US-09-988-493-133
2	40	100.0	10	14	US-10-014-340-427
3	40	100.0	10	14	US-10-014-340-428
4	40	100.0	10	15	US-10-203-334-2
5	40	100.0	10	15	US-10-601-837-131
6	40	100.0	10	16	US-10-700-330-140
7	40	100.0	199	9	US-09-864-761-34284
8	40	100.0	261	15	US-10-424-599-185342
9	40	100.0	302	15	US-10-424-599-181988
10	40	100.0	332	14	US-10-103-313-367
11	40	100.0	351	9	US-09-864-761-33332

12	40	100.0	355	15	US-10-369-493-12369	Sequence 12369, A
13	40	100.0	435	15	US-10-250-613-7	Sequence 7, Appl
14	40	100.0	441	15	US-10-369-493-6833	Sequence 6833, Ap
15	40	100.0	444	15	US-10-369-493-6856	Sequence 6856, Ap
16	40	100.0	444	15	US-10-439-616-10	Sequence 10, Appl
17	40	100.0	444	15	US-10-439-616-11	Sequence 11, Appl
18	40	100.0	444	15	US-10-439-616-12	Sequence 12, Appl
19	40	100.0	444	15	US-10-439-616-13	Sequence 13, Appl
20	40	100.0	444	15	US-10-439-616-14	Sequence 14, Appl
21	40	100.0	444	15	US-10-439-616-15	Sequence 15, Appl
22	40	100.0	444	15	US-10-439-616-24	Sequence 24, Appl
23	40	100.0	444	15	US-10-439-616-25	Sequence 25, Appl
24	40	100.0	444	15	US-10-439-616-26	Sequence 26, Appl
25	40	100.0	444	15	US-10-439-616-27	Sequence 27, Appl
26	40	100.0	444	15	US-10-439-616-28	Sequence 28, Appl
27	40	100.0	444	15	US-10-439-616-29	Sequence 29, Appl
28	40	100.0	444	15	US-10-439-616-30	Sequence 30, Appl
29	40	100.0	444	15	US-10-439-616-31	Sequence 31, Appl
30	40	100.0	444	15	US-10-439-616-39	Sequence 39, Appl
31	40	100.0	444	15	US-10-439-616-40	Sequence 40, Appl
32	40	100.0	444	15	US-10-439-616-41	Sequence 41, Appl
33	40	100.0	444	15	US-10-439-616-42	Sequence 42, Appl
34	40	100.0	444	15	US-10-439-616-43	Sequence 43, Appl
35	40	100.0	444	15	US-10-439-616-44	Sequence 44, Appl
36	40	100.0	444	15	US-10-439-616-45	Sequence 45, Appl
37	40	100.0	444	15	US-10-205-331-112	Sequence 112, App
38	40	100.0	444	16	US-10-408-765A-680	Sequence 680, App
39	40	100.0	444	16	US-10-408-765A-2132	Sequence 2132, Ap
40	40	100.0	444	16	US-10-370-715B-130	Sequence 130, App
41	40	100.0	444	17	US-10-734-049A-240	Sequence 240, App
42	40	100.0	445	14	US-10-205-219-145	Sequence 145, App
43	40	100.0	445	16	US-10-408-765A-806	Sequence 806, App
44	40	100.0	445	16	US-10-788-792-167	Sequence 167, App
45	40	100.0	449	15	US-10-369-493-5888	Sequence 5888, Ap

ALIGNMENTS

RESULT 1
US-09-988-493-133
; Sequence 133, Application US/09988493
; Publication No. US20030064119A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: O'Hare, Michael John
; APPLICANT: Page, Martin John
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Waterfield, Michael Derek
; TITLE OF INVENTION: Proteins, Genes, and Their Use for
; TITLE OF INVENTION: Diagnosis, Genes, and Their Use for
; FILE REFERENCE: 2543-1-024
; CURRENT APPLICATION NUMBER: US/09/988,493
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/GB01/01219
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: GB 0006695.1
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: GB 0007265.2
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapien
US-09-988-493-133

Query Match 100.0%; Score 40; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NMVPPFR 7

Db 4 NMVPFPR 10
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RESULT 2

US-10-014-340-427
; Sequence 427, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 427
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-427

Query Match 100.0%; Score 40; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
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Db 4 NMVPFPR 10
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RESULT 3

US-10-014-340-428
; Sequence 428, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 428
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-428

Query Match 100.0%; Score 40; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
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Db 4 NMVPFPR 10
|||||

RESULT 4

US-10-203-334-2
; Sequence 2, Application US/10203334
; Publication No. US20040038417A1
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft zur Forderung der Wissenschaften e.V.
; APPLICANT: CARILL, DOLORES, J.
; APPLICANT: NORDHOFF, ECKHARD
; APPLICANT: KLOSE, JOACHIM
; APPLICANT: EICKHOFF, HOLGER
; APPLICANT: SCHMIDT, FRANK
; APPLICANT: LEHRACH, HANS
; TITLE OF INVENTION: Method for identifying and/or characterizing a (poly)peptide

; FILE REFERENCE: 009848-0272307
; CURRENT APPLICATION NUMBER: US/10/203,334
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/EP01/01332
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: EP 00 10 2567.5
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-334-2

Query Match 100.0%; Score 40; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
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Db 4 NMVPFPR 10
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RESULT 5

US-10-601-837-131
; Sequence 131, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
; APPLICANT: Moyses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidne
; TITLE OF INVENTION: Response
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Ratus No. US20040053309Alvegicus
US-10-601-837-131

Query Match 100.0%; Score 40; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
|||||

Db 4 NMVPFPR 10
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RESULT 6

US-10-700-330-140
; Sequence 140, Application US/10700330
; Publication No. US20040203022A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Mudiyansele Athula Chandrasiri Herath
; APPLICANT: Page, Martin John
; TITLE OF INVENTION: Proteins and Genes For Diagnosis And Treatment of Erbb2-Related Ca
; FILE REFERENCE: 2543-1-031
; CURRENT APPLICATION NUMBER: US/10/700,330
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: GB 0110886.9
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: GB 0128183.1

; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-330-140

Query Match 100.0%; Score 40; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.47; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 4 NMVPFPR 10
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RESULT 7

US-09-864-761-34284
; Sequence 34284, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34284
; LENGTH: 199
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF146191.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 37
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 32
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 38
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 51
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 59
; OTHER INFORMATION: EST HUMAN HIT: BE791523.1, EVALUE 1.00e-100
; OTHER INFORMATION: SWISSPROT HIT: P30883, EVALUE 1.00e-101
US-09-864-761-34284

Query Match 100.0%; Score 40; DB 9; Length 199;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 34 NMVPFPR 40
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RESULT 8

US-10-424-599-185342
; Sequence 185342, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 185342
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138379C.1.pep
US-10-424-599-185342

Query Match 100.0%; Score 40; DB 15; Length 261;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 71 NMVPFPR 77
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RESULT 9

US-10-424-599-181988
; Sequence 181988, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684

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; SEQ ID NO 181988
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(302)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135349C.1.pep
US-10-424-599-181988

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Query Match          100.0%; Score 40; DB 15; Length 302;
Best Local Similarity 100.0%; Pred. No. 14; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

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Qy      1 NMVPPFR 7
Db      111 NMVPPFR 117

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RESULT 10
US-10-103-313-367
; Sequence 367, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 367
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-313-367

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Query Match          100.0%; Score 40; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 16; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

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Qy      1 NMVPPFR 7
Db      142 NMVPPFR 148

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RESULT 11
US-09-864-761-33332
; Sequence 33332, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

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; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33332
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023051.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 51
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 51
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1e+02
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 30
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 23
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9
; OTHER INFORMATION: EST HUMAN HIT: BE745540.1, EVALUAE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: A1815647.1, EVALUAE 1.00e-125
; OTHER INFORMATION: SWISSPROT HIT: P05218, EVALUAE 0.00e+00
US-09-864-761-33332

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Query Match          100.0%; Score 40; DB 9; Length 351;
Best Local Similarity 100.0%; Pred. No. 16; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

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Qy      1 NMVPPFR 7
Db      163 NMVPPFR 169

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RESULT 12
US-10-369-493-123369
; Sequence 12369, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28

```

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; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12369
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(355)
; OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-12369

Query Match      100.0%; Score 40; DB 15; Length 355;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NMVPPFR 7
Db      139 NMVPPFR 145

RESULT 13
US-10-250-613-7
; Sequence 7, Application US/10250613
; Publication No. US20040096828A1
; GENERAL INFORMATION:
; APPLICANT: LU, Dyung Aina M.; BAUGHN, Mariah R.;
; APPLICANT: YAO, Monique G.; DING, Li;
; APPLICANT: HONCHELL, Cynthia D.; YUE, Henry;
; APPLICANT: TANG, Y. Tom; WARREN, Bridget A.;
; APPLICANT: DUGGAN, Brendan M.; XU, Yuming;
; APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
; APPLICANT: STEWART, Elizabeth A.; GANDHI, Ameena R.;
; APPLICANT: KHAN, Farrah A.; THANGAVELU, Kavitha;
; APPLICANT: ISON, Craig H.; AZIMZAI, Yalda;
; APPLICANT: HAFALIA, April J.A.; GIFTZEN, Kimberly J.;
; APPLICANT: LAL, Preeti G.; SANJANWALA, Madhusudan M.;
; APPLICANT: ELLIOTT, Vicki S.
; TITLE OF INVENTION: CYTOSKELETAL-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0878 USN
; CURRENT APPLICATION NUMBER: US/10/250,613
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: PCT/US02/00178
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,085
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: US 60/268,554
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/269,111
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 60/271,211
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7484690CD1
US-10-250-613-7

Query Match      100.0%; Score 40; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NMVPPFR 7
Db      257 NMVPPFR 263

RESULT 14
US-10-369-493-6833
; Sequence 6833, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6833
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6833

Query Match      100.0%; Score 40; DB 15; Length 441;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NMVPPFR 7
Db      256 NMVPPFR 262

RESULT 15
US-10-369-493-6856
; Sequence 6856, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6856
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6856

Query Match      100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NMVPPFR 7
Db      256 NMVPPFR 262

RESULT 16
US-10-439-616-10
; Sequence 10, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF FACILITAXEL RESISTANT CELLS IN HUMAN TUN
```

; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (215)..(215)
; OTHER INFORMATION: 215 Leu to His variant
US-10-439-616-10

Query Match 100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| | | | |
Db 256 NMVPPFR 262

RESULT 17
US-10-439-616-11
; Sequence 11, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (215)..(215)
; OTHER INFORMATION: 215 Leu to Arg variant
US-10-439-616-11

Query Match 100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| | | | |
Db 256 NMVPPFR 262

RESULT 18
US-10-439-616-12
; Sequence 12, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16

; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (215)..(215)
; OTHER INFORMATION: 215 Leu to Phe variant
US-10-439-616-12

Query Match 100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| | | | |
Db 256 NMVPPFR 262

RESULT 19
US-10-439-616-13
; Sequence 13, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (217)..(217)
; OTHER INFORMATION: 217 Leu to Arg variant
US-10-439-616-13

Query Match 100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
| | | | |
Db 256 NMVPPFR 262

RESULT 20
US-10-439-616-14
; Sequence 14, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099

; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (228)..(228)
 ; OTHER INFORMATION: 228 Leu to Phe variant
 US-10-439-616-14

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
 Db 256 NMVPFPR 262

RESULT 21
 US-10-439-616-15
 ; Sequence 15, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (228)..(228)
 ; OTHER INFORMATION: 228 Leu to His variant
 US-10-439-616-15

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
 Db 256 NMVPFPR 262

RESULT 22
 US-10-439-616-24
 ; Sequence 24, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 24
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (214)..(214)
 ; OTHER INFORMATION: 214 Thr to Ala variant
 US-10-439-616-24

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
 Db 256 NMVPFPR 262

RESULT 23
 US-10-439-616-25
 ; Sequence 25, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 25
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (215)..(215)
 ; OTHER INFORMATION: 215 Leu to Ala variant
 US-10-439-616-25

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPFPR 7
 Db 256 NMVPFPR 262

RESULT 24
 US-10-439-616-26
 ; Sequence 26, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 26
 ; LENGTH: 444
 ; TYPE: PRT

```

; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (215 )..(215 )
; OTHER INFORMATION: 215 Leu to Glu variant
US-10-439-616-26

Query Match      100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 25
US-10-439-616-27
; Sequence 27, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (215 )..(215 )
; OTHER INFORMATION: 215 Leu to Met variant
US-10-439-616-27

Query Match      100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 26
US-10-439-616-28
; Sequence 28, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant

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; LOCATION: (215 )..(215 )
; OTHER INFORMATION: 215 Leu to Pro variant
US-10-439-616-28

Query Match      100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 27
US-10-439-616-29
; Sequence 29, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (216 )..(216 )
; OTHER INFORMATION: 216 Lys to Ala variant
US-10-439-616-29

Query Match      100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 28
US-10-439-616-30
; Sequence 30, Application US/10439616
; Publication No. US20030235855A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
; FILE REFERENCE: 96606/05CIP
; CURRENT APPLICATION NUMBER: US/10/439,616
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: 60/135047
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574099
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: variant
; LOCATION: (217 )..(217 )
; OTHER INFORMATION: 217 Leu to Ala variant
US-10-439-616-30

```

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
 DB 256 NMVPPPR 262

RESULT 29
 US-10-439-616-31
 ; Sequence 31, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (228)..(228)
 ; OTHER INFORMATION: 228 Leu to Ala variant
 US-10-439-616-31

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
 DB 256 NMVPPPR 262

RESULT 30
 US-10-439-616-39
 ; Sequence 39, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 39
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (210)..(210)
 ; OTHER INFORMATION: 210 Ile to Thr variant
 US-10-439-616-39

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
 DB 256 NMVPPPR 262

RESULT 31
 US-10-439-616-40
 ; Sequence 40, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 40
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (217)..(217)
 ; OTHER INFORMATION: 217 Leu to Apn variant
 US-10-439-616-40

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
 DB 256 NMVPPPR 262

RESULT 32
 US-10-439-616-41
 ; Sequence 41, Application US/10439616
 ; Publication No. US20030235855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Texas System
 ; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU
 ; FILE REFERENCE: 96606/05CIP
 ; CURRENT APPLICATION NUMBER: US/10/439,616
 ; CURRENT FILING DATE: 2003-05-16
 ; PRIOR APPLICATION NUMBER: 60/135047
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/574099
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 41
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (270)..(270)
 ; OTHER INFORMATION: 270 Phe to Cys variant
 US-10-439-616-41

Query Match 100.0%; Score 40; DB 15; Length 444;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7

Db 256 NMVPPFR 262
|||||

RESULT 33

US-10-439-616-42

; Sequence 42, Application US/10439616

; Publication No. US20030235855A1

; GENERAL INFORMATION:

; APPLICANT: Board of Regents of the University of Texas System

; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU

; FILE REFERENCE: 96606/05CIP

; CURRENT APPLICATION NUMBER: US/10/439,616

; CURRENT FILING DATE: 2003-05-16

; PRIOR APPLICATION NUMBER: 60/135047

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/574099

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 42

; LENGTH: 444

; TYPE: PRT

; ORGANISM: Cricetus griseus

; FEATURE:

; NAME/KEY: variant

; LOCATION: (292)..(292)

; OTHER INFORMATION: 292 Gln to His variant

US-10-439-616-42

Query Match 100.0%; Score 40; DB 15; Length 444;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
|||||

Db 256 NMVPPFR 262
|||||

RESULT 34

US-10-439-616-43

; Sequence 43, Application US/10439616

; Publication No. US20030235855A1

; GENERAL INFORMATION:

; APPLICANT: Board of Regents of the University of Texas System

; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU

; FILE REFERENCE: 96606/05CIP

; CURRENT APPLICATION NUMBER: US/10/439,616

; CURRENT FILING DATE: 2003-05-16

; PRIOR APPLICATION NUMBER: 60/135047

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/574099

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 43

; LENGTH: 444

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: variant

; LOCATION: (225)..(225)

; OTHER INFORMATION: 225 Leu to Met variant

US-10-439-616-43

Query Match 100.0%; Score 40; DB 15; Length 444;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
|||||

Db 256 NMVPPFR 262
|||||

RESULT 35

US-10-439-616-44

; Sequence 44, Application US/10439616

; Publication No. US20030235855A1

; GENERAL INFORMATION:

; APPLICANT: Board of Regents of the University of Texas System

; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU

; FILE REFERENCE: 96606/05CIP

; CURRENT APPLICATION NUMBER: US/10/439,616

; CURRENT FILING DATE: 2003-05-16

; PRIOR APPLICATION NUMBER: 60/135047

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/574099

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 44

; LENGTH: 444

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: variant

; LOCATION: (273)..(273)

; OTHER INFORMATION: 273 Leu to Val variant

US-10-439-616-44

Query Match 100.0%; Score 40; DB 15; Length 444;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
|||||

Db 256 NMVPPFR 262
|||||

RESULT 36

US-10-439-616-45

; Sequence 45, Application US/10439616

; Publication No. US20030235855A1

; GENERAL INFORMATION:

; APPLICANT: Board of Regents of the University of Texas System

; TITLE OF INVENTION: ASSAY FOR THE DETECTION OF PACLITAXEL RESISTANT CELLS IN HUMAN TU

; FILE REFERENCE: 96606/05CIP

; CURRENT APPLICATION NUMBER: US/10/439,616

; CURRENT FILING DATE: 2003-05-16

; PRIOR APPLICATION NUMBER: 60/135047

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/574099

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 45

; LENGTH: 444

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: variant

; LOCATION: (365)..(365)

; OTHER INFORMATION: 365 Val to Asp variant

US-10-439-616-45

Query Match 100.0%; Score 40; DB 15; Length 444;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
|||||

Db 256 NMVPPFR 262
|||||

RESULT 37

US-10-205-331-112

; Sequence 112, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnoch, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Class 1 beta tubulin
US-10-205-331-112

Query Match 100.0%; Score 40; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 38
US-10-408-765A-680
; Sequence 680, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 680
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-680

Query Match 100.0%; Score 40; DB 16; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 39
US-10-408-765A-2132
; Sequence 2132, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2132
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2132

Query Match 100.0%; Score 40; DB 16; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 40
US-10-370-715B-130
; Sequence 130, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILGARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: PI948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 130
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-130

Query Match 100.0%; Score 40; DB 16; Length 444;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

Search completed: July 20, 2005, 17:50:19
Job time : 57.5185 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 17:20:08 ; Search time 12.1852 Seconds
(without alignments)
55.273 Million cell updates/sec

Title: US-10-766-480A-1

Perfect score: 40

Sequence: 1 NMVPPFR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	163	2 S39818	tubulin beta-1 cha
2	40	100.0	163	2 S39820	tubulin beta-3 cha
3	40	100.0	163	2 S39819	tubulin beta-2 cha
4	40	100.0	219	2 S55460	beta-tubulin - nem
5	40	100.0	224	2 S67949	beta-tubulin ASL1
6	40	100.0	292	2 S02327	tubulin beta chain
7	40	100.0	321	2 B25437	tubulin beta-2 cha
8	40	100.0	360	2 S18458	tubulin beta chain
9	40	100.0	437	2 I38369	beta-tubulin - hum
10	40	100.0	441	2 S05956	tubulin beta-2 cha
11	40	100.0	441	2 S45071	tubulin beta chain
12	40	100.0	442	2 S20908	tubulin beta chain
13	40	100.0	443	2 S05968	tubulin beta-2 cha
14	40	100.0	444	1 UBHUB	tubulin beta chain
15	40	100.0	444	2 D25437	tubulin beta-4 cha
16	40	100.0	444	2 S01713	tubulin beta-7 cha
17	40	100.0	444	2 A26561	tubulin beta chain
18	40	100.0	444	2 T18683	hypothetical prote
19	40	100.0	444	2 S18457	tubulin beta chain
20	40	100.0	444	2 S18456	tubulin beta chain
21	40	100.0	444	2 E25437	tubulin beta-5 cha
22	40	100.0	444	2 S35191	tubulin beta-1 cha
23	40	100.0	445	1 UBCHB	tubulin beta chain
24	40	100.0	445	1 UBPGH	tubulin beta chain
25	40	100.0	445	2 A25113	tubulin beta chain
26	40	100.0	445	2 B45794	tubulin beta chain
27	40	100.0	445	2 A24701	tubulin beta-3 cha
28	40	100.0	445	2 I50435	beta-1 tubulin - c
29	40	100.0	445	2 I38370	beta-tubulin - hum

```

30 40 100.0 445 2 T08726 tubulin beta chain
31 40 100.0 445 2 S37144 tubulin beta chain
32 40 100.0 445 2 C25437 tubulin beta-3 cha
33 40 100.0 445 2 JC7788 beta-tubulin - bas
34 40 100.0 446 2 A27810 tubulin beta-2 cha
35 40 100.0 446 2 B27554 tubulin beta-5 cha
36 40 100.0 446 2 A27424 tubulin beta chain
37 40 100.0 446 2 S08403 tubulin beta chain
38 40 100.0 446 2 A48407 neural class-II be
39 40 100.0 446 2 S25554 tubulin beta chain
40 40 100.0 447 2 S49328 tubulin beta-2 cha
41 40 100.0 447 2 JQ0423 tubulin beta chain
42 40 100.0 447 2 S05429 tubulin beta chain
43 40 100.0 447 2 JQ0171 tubulin beta chain
44 40 100.0 447 2 S17729 tubulin beta chain
45 40 100.0 447 2 S17730 tubulin beta chain

```

ALIGNMENTS

RESULT 1

S39818

tubulin beta-1 chain - fruit fly (Drosophila melanogaster) (fragment)

C:Species: Drosophila melanogaster

C>Date: 06-Feb-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S39818

R:Scouras, Z.G.; Milloni, D.; Yiangou, M.; Duchene, M.; Domdey, H.

Curr. Genet. 25, 84-87, 1994

A:Title: The beta-tubulin genes of Drosophila auraria are arranged in a cluster.

A:Reference number: S39818; MUID:94363742; PMID:8082170

A:Accession: S39818

A:Molecule type: DNA

A:Residues: 1-163 <SCO>

A:Cross-references: UNIPROT:Q7M3K1

C:Genetics:

A:Gene: FlyBase:beta-Tub56D

A:Cross-references: FlyBase:FBgn0003887

C:Superfamily: tubulin

Query Match

Best Local Similarity 100.0%; Score 40; DB 2; Length 163;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NMVPPFR 7

Db 101 NMVPPFR 107

RESULT 2

S39820

tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)

C:Species: Drosophila melanogaster

C>Date: 06-Feb-1995 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S39820

R:Scouras, Z.G.; Milloni, D.; Yiangou, M.; Duchene, M.; Domdey, H.

Curr. Genet. 25, 84-87, 1994

A:Title: The beta-tubulin genes of Drosophila auraria are arranged in a cluster.

A:Reference number: S39818; MUID:94363742; PMID:8082170

A:Accession: S39820

A:Molecule type: DNA

A:Residues: 1-163 <SCO>

A:Cross-references: UNIPROT:Q7M3J9

C:Genetics:

A:Gene: FlyBase:beta-Tub60D

A:Cross-references: FlyBase:FBgn0003888

C:Superfamily: tubulin

Query Match

Best Local Similarity 100.0%; Score 40; DB 2; Length 163;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NMVPPFR 7

Db 101 NMVPPFR 107
|||||
RESULT 3
tubulin beta-2 chain - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 19-May-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S39819
R:Scouras, Z.G.; Milioni, D.; Yiangou, M.; Duchene, M.; Domdey, H.
Curr. Genet. 25, 84-87, 1994
A:Title: The beta-tubulin genes of Drosophila auraria are arranged in a cluster.
A:Reference number: S39818; MUID:94363742; PMID:8082170
A:Accession: S39819
A:Molecule type: DNA
A:Residues: 1-163 <SCO>
A:Cross-references: UNIPROT:O7M3K0
A:Note: the authors translated the codon GGC for residue 76 as Ala
C:Genetics:
A:Gene: FlyBase:beta-Tub85D
A:Cross-references: FlyBase:FBgn0003889
C:Superfamily: tubulin
Query Match 100.0%; Score 40; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.64; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
Qy 1 NMVPPFR 7
|||||
Db 101 NMVPPFR 107
RESULT 4
S55460
beta-tubulin - nematode (Haemonchus contortus) (fragment)
C:Species: Haemonchus contortus
C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S55460
R:Roos, M.H.
submitted to the EMBL Data Library, July 1992
A:Reference number: S55460
A:Accession: S55460
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <ROO>
A:Cross-references: UNIPROT:Q25038; EMBL:X67487; NID:g853957; PIDN:CAA47827.1; PID:g853957
C:Superfamily: tubulin
Query Match 100.0%; Score 40; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.86; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
Qy 1 NMVPPFR 7
|||||
Db 27 NMVPPFR 33
RESULT 5
S67949
beta-tubulin ASL1 - nematode (Haemonchus contortus) (fragment)
C:Species: Haemonchus contortus
C>Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S67949
R:Roos, M.H.; Grant, W.N.
Int. J. Parasitol. 23, 419-421, 1993
A:Title: Species-specific PCR for the parasitic nematodes Haemonchus contortus and Trichostrongylus axei
A:Reference number: S67949; MUID:93366546; PMID:8359994
A:Accession: S67949
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <ROO>
A:Cross-references: UNIPROT:Q08950; EMBL:X67485; NID:g396690; PIDN:CAA47825.1; PID:g396690

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Genetics:
A:Gene: ASL-1
A:Introns: 6/1; 69/3; 101/3; 163/3; 202/3
C:Superfamily: tubulin
Query Match 100.0%; Score 40; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.88; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
Qy 1 NMVPPFR 7
|||||
Db 33 NMVPPFR 39
RESULT 6
S02327
tubulin beta chain - sea urchin (Strongylocentrotus purpuratus) (fragment)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S02327
R:Harlow, P.; Litwin, S.; Nemer, M.
J. Mol. Evol. 27, 56-64, 1988
A:Title: Synonymous nucleotide substitution rates of beta-tubulin and histone genes conf
A:Reference number: S02327; MUID:88259239; PMID:3133488
A:Accession: S02327
A:Molecule type: mRNA
A:Residues: 1-292 <HAR>
A:Cross-references: UNIPROT:P18700; EMBL:X07502; NID:g10329; PIDN:CAA30385.1; PID:g13356;
C:Superfamily: tubulin
Query Match 100.0%; Score 40; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;
Qy 1 NMVPPFR 7
|||||
Db 101 NMVPPFR 107
RESULT 7
B25437
tubulin beta-2 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 09-Jul-2004
C:Accession: B25437; S29015; S48742
R:Wang, D.; Villalante, A.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 103, 1903-1910, 1986
A:Title: The mammalian beta-tubulin repertoire: hematopoietic expression of a novel, heter
A:Reference number: A92746; MUID:87057644; PMID:3782288
A:Accession: B25437
A:Molecule type: mRNA
A:Residues: 1-321 <WAN>
A:Cross-references: UNIPROT:Q62363
A:Note: the authors translated the codon ATG for residue 45 as Val and GTG for residue 46
R:Lewis, S.A.; Lee, M.G.S.; Cowan, N.J.
J. Cell Biol. 101, 852-861, 1985
A:Title: Five mouse tubulin isotypes and their regulated expression during development.
A:Reference number: S29013; MUID:85289512; PMID:3839797
A:Accession: S29015
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 22-275, A', 277-321 <LEW>
A:Cross-references: EMBL:M28739; NID:g202226; PIDN:AAA40508.1; PID:g202227
A:Note: the authors translated the codon GCT for residue 276 as Gly
R:Mary, J.; Redeker, V.; le Caer, J.P.; Prome, J.C.; Rossier, J.
FEBS Lett. 353, 89-94, 1994
A:Title: Class I and IVa beta-tubulin isotypes expressed in adult mouse brain are glutamyl
A:Reference number: S48741; MUID:95010772; PMID:7926030
A:Accession: S48742
A>Status: preliminary
A:Molecule type: protein
A:Residues: 303-321 <MAR>

C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 NMVPPFR 7
DB 132 NMVPPFR 138

RESULT 8

S18458
tubulin beta chain (clone 9T) - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S18458
R:Ahmad, S.; Singh, B.; Gupta, R.S.
Biochim. Biophys. Acta 1090, 252-254, 1991
A:Title: Nucleotide sequences of three different isoforms of beta-tubulin cDNA from Chin
A:Reference number: S18456; MUID:92031702; PMID:1657186
A:Accession: S18458
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-360 <ARM>
A:Cross-references: UNIPROT:Q60456; GB:X60786; NID:9537408; PIDN:CAA43199.1; PID:9537409
C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 NMVPPFR 7
DB 169 NMVPPFR 175

RESULT 9

138369
beta-tubulin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 13-Aug-1999
C:Accession: 138369
R:Hall, J.L.; Dudley, L.; Dobner, P.R.; Lewis, S.A.; Cowan, N.J.
Mol. Cell. Biol. 3, 854-862, 1983
A:Title: Identification of two human beta-tubulin isoatypes.
A:Reference number: 138369; MUID:83244582; PMID:6865944
A:Accession: 138369
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-437 <RES>
A:Cross-references: EMBL:V00599; NID:937490; PIDN:CAA23844.1; PID:9897763
C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 NMVPPFR 7
DB 249 NMVPPFR 255

RESULT 10

S05956
tubulin beta-2 chain - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S05956; #25982
R:Savage, C.; Hamelin, M.; Culotti, J.G.; Coulson, A.; Albertson, D.G.; Chalfie, M.
Genes Dev. 3, 870-881, 1989
A:Title: mec-7 is a beta-tubulin gene required for the production of 15-protot filament mi
A:Reference number: S05956; MUID:89306623; PMID:2744465

A:Accession: S05956
A:Molecule type: DNA
A:Residues: 1-441 <SAV>
A:Cross-references: UNIPROT:P12456; EMBL:X15242; NID:96891; PIDN:CAA33320.1; PID:96892
R:Connell, M.
submitted to the EMBL Data Library, September 1996
A:Description: The sequence of C. elegans cosmid ZK154.
A:Reference number: Z20119
A:Accession: T25982
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-441 <CON>
A:Cross-references: EMBL:U70844; PIDN:AAB09092.1; GSPDB:GN00028; CESP:mec-7
A:Experimental source: strain Bristol N2; clone ZK154
C:Genetics:
A:Gene: tub-2; mec-7
A:Map position: X
A:Introns: 19/3; 62/2; 280/3; 387/1
C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 NMVPPFR 7
DB 256 NMVPPFR 262

RESULT 11

S45071
tubulin beta chain - common limpet
C:Species: Patella vulgata (Common limpet)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S45071
R:van Loon, A.E.; Goedemans, H.J.; Weiftens, M.E.M.; Daemen, A.J.J.M.
submitted to the EMBL Data Library, May 1994
A:Description: Onset of transcription in Patella vulgata coincides with cell cycle elonga
A:Reference number: S45070
A:Accession: S45071
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-441 <VAN>
A:Cross-references: UNIPROT:Q26165; EMBL:X79469; NID:9496496; PIDN:CAA55979.1; PID:913356
C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 NMVPPFR 7
DB 252 NMVPPFR 258

RESULT 12

S20908
tubulin beta chain - Pneumocystis carinii
C:Species: Pneumocystis carinii
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S20908; S28432; PN0596; S17110
R:Dyer, M.; Volpe, F.; Delves, C.J.; Somia, N.; Burns, S.; Scaife, J.G.
Mol. Microbiol. 6, 991-1001, 1992
A:Title: Cloning and sequence of a beta-tubulin cDNA from Pneumocystis carinii: possible
A:Reference number: S20908; MUID:92261328; PMID:1584027
A:Accession: S20908

A:Molecule type: mRNA

A:Residues: 1-442 <DYB>
A:Cross-references: UNIPROT:P24637; EMBL:X62113; NID:99813; PIDN:CAA44023.1; PID:99814
R:Edling, T.D.; Bartlett, M.S.; Weinberg, G.A.; Prah, G.N.; Smith, J.W.
Mol. Microbiol. 6, 3365-3373, 1992
A:Title: The beta-tubulin gene from rat and human isolates of Pneumocystis carinii.
A:Reference number: S28432; MUID:93133116; PMID:1484490

A;Accession: S28432
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-442 <EDL>
A;Cross-references: GB:L05466; NID:g169399; PIDN:AAA33786.1; PID:g169400
R;Fletcher, L.D.; Berger, L.C.; Peel, S.A.; Baric, R.S.; Tidwell, R.R.; Dykstra, C.C.
Gene 129, 167-174, 1993
A;Title: Isolation and identification of six Pneumocystis carinii genes utilizing codon
A;Reference number: FN0595; MUID:93314959; PMID:8325503
A;Accession: FN0596
A;Molecule type: DNA
A;Residues: 96-208 <FLE>
A;Cross-references: GB:M96932; NID:g169401; PIDN:AAA02566.1; PID:g169402
C;Genetics:
A;Introns: 190/3
C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 NMVPPPR 7
Db 256 NMVPPPR 262

RESULT 13
S05968
tubulin beta-2 chain - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
A;Accession: S05968
R;Good, P.J.; Richter, K.; Dawid, I.B.
Nucleic Acids Res. 17, 8000, 1989
A;Title: The sequence of a nervous system-specific, class II beta-tubulin gene from Xenopus laevis
A;Reference number: S05968; MUID:90016895; PMID:2798144
A;Accession: S05968
A;Molecule type: mRNA
A;Residues: 1-443 <GOO>
A;Cross-references: UNIPROT:P13602; EMBL:X15798; NID:g65168; PIDN:CAA33798.1; PID:g65169
C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 NMVPPPR 7
Db 256 NMVPPPR 262

RESULT 14
UBHUSB
tubulin beta chain - human
N;Alternate names: 5-beta tubulin
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
A;Accession: A02972
R;Lee, M.G.S.; Loomis, C.; Cowan, N.J.
Nucleic Acids Res. 12, 5823-5836, 1984
A;Title: Sequence of an expressed human beta-tubulin gene containing ten Alu family members
A;Reference number: A02972; MUID:84272256; PMID:6462917
A;Accession: A02972
A;Molecule type: DNA
A;Residues: 1-444 <LEE>
A;Cross-references: UNIPROT:P04350; GB:X00734; NID:g35958; PIDN:CAA25318.1; PID:g35959
A;Note: the authors translated the codon AAT for residue 58 as Lys and ATG for residue 118 as Met.
C;Comment: Tubulin is a dimer of alpha and beta chains and is found in the microtubules
changeable site on its beta chain and at a nonexchangeable site not yet identified.
C;Comment: The highly acidic carboxyl-terminal region may bind cations such as calcium.
C;Comment: Although the majority of the human beta tubulin genes are pseudogenes lacking
expressed in the same cell, it is not known if both are assembled into the same microtubule.
C;Genetics:

A;Gene: GDB:TUBB
A;Cross-references: GDB:119622; OMIM:191130
A;Map position: 6p21.3-6p21.3
A;Introns: 19/3; 56/1; 93/1
C;Superfamily: tubulin
C;Keywords: microtubule
F;140-146/Region: tubulin/FtsZ GTP/GDP-binding (G-G-T-G-[ST]-G) motif

Query Match 100.0%; Score 40; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 NMVPPPR 7
Db 256 NMVPPPR 262

RESULT 15
D25437
tubulin beta-4 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 13-Aug-1999
C;Accession: D25437; S29016; S34783; S48744
R;Wang, D.; Villalante, A.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 103, 1903-1910, 1986
A;Title: The mammalian beta-tubulin repertoire: hematopoietic expression of a novel, heterologous beta-tubulin
A;Reference number: A92746; MUID:87057644; PMID:3782288
A;Accession: D25437
A;Molecule type: mRNA
A;Residues: 1-444 <WAN>
R;Lewis, S.A.; Lee, M.G.S.; Cowan, N.J.
J. Cell Biol. 101, 852-861, 1985
A;Title: Five mouse tubulin isotypes and their regulated expression during development.
A;Reference number: S29013; MUID:85289512; PMID:3839797
A;Accession: S29016
A;Molecule type: mRNA
A;Residues: 66-72, 'I', 74-110, 'Q', 112-292, 'V', 294-302, 'S', 304-350, 'A', 352-399, 'A', 401-444
A;Cross-references: EMBL:M28730
A;Note: the authors translated the codon ATC for residue 73 as Met, GAG for residue 181 as Glu, and GAG for residue 181 as Gly
R;Lewis, S.A.; Lee, M.G.S.; Cowan, N.J.
submitted to the EMBL Data Library, August 1990
A;Description: Five mouse tubulin isotypes and their regulated expression during development
A;Reference number: S34783
A;Accession: S34783
A;Molecule type: mRNA
A;Residues: 66-72, 'I', 74-110, 'Q', 112-269, 'L', 271-292, 'V', 294-302, 'S', 304-350, 'A', 352-399, 'A', 401-444
A;Cross-references: EMBL:M28730; NID:g202228; PIDN:AAA40509.1; PID:g202229
R;Mary, J.; Redeker, V.; le Caer, J.P.; Prome, J.C.; Rossier, J.
FEBS Lett. 353, 89-94, 1994
A;Title: Class I and IV beta-tubulin isotypes expressed in adult mouse brain are glutamylated
A;Reference number: S48741; MUID:95010772; PMID:7926030
A;Accession: S48744
A;Status: preliminary
A;Molecule type: protein
A;Residues: 426-444 <MAR>
C;Superfamily: tubulin
C;Keywords: microtubule

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 NMVPPPR 7
Db 256 NMVPPPR 262

RESULT 16
S01713
tubulin beta-7 chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: S01713
R;Monteiro, M.J.; Cleveland, D.W.
J. Mol. Biol. 199, 439-446, 1988
A;Title: Sequence of chicken c-beta-7 tubulin. Analysis of a complete set of vertebrate
A;Reference number: S01713; MUID:88172491; PMID:3351937
A;Accession: S01713
A;Molecule type: mRNA
A;Residues: 1-444 <NM>
C;Cross-references: UNIPROT:P09244; EMBL:X07011; NID:G63166; PIDN:CAA30060.1; PID:G63167
C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
|||||
Db 256 NMVPPPR 262

RESULT 17
A26561
tubulin beta chain - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 09-Jul-2004
C;Accession: A26561
R;Lee, M.G.S.; Lewis, S.A.; Wilde, C.D.; Cowan, N.J.
Cell 33, 477-487, 1983
A;Reference number: A26561; MUID:83232883; PMID:6688039
A;Accession: A26561
A;Molecule type: mRNA
A;Residues: 1-444 <LEE>
A;Cross-references: UNIPROT:P07437; GB:J00314; NID:G338694; PIDN:AAB59507.1; PID:G338695
A;Note: the authors translated the codon GAG for residue 111 as Gly
C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
|||||
Db 256 NMVPPPR 262

RESULT 18
T18683
hypochemical protein B0272.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18683
R;Sulston, J.
submitted to the EMBL Data Library, October 1994
A;Reference number: Z19006
A;Accession: T18683
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-444 <WIL>
A;Cross-references: UNIPROT:P41937; EMBL:Z46240; NID:G559408; PIDN:CAA86310.1; GSPDB:GNC
A;Experimental source: clone B0272
C;Genetics:
A;Gene: CESP:B0272.1
A;Map position: X
A;Introns: 19/3; 56/1; 131/3; 245/3; 282/2; 387/1
C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
|||||
Db 256 NMVPPPR 262

RESULT 19
S18457
tubulin beta chain (clone 3T) - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S18457
R;Ahmad, S.; Singh, B.; Gupta, R.S.
Biochim. Biophys. Acta 1090, 252-254, 1991
A;Title: Nucleotide sequences of three different isoforms of beta-tubulin cDNA from Chinese hamster ovary cells
A;Reference number: S18456; MUID:92031702; PMID:1657186
A;Accession: S18457
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-444 <AHM>
A;Cross-references: UNIPROT:Q60455; GB:X60785; NID:G537406; PIDN:CAA43198.1; PID:G537407
C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
|||||
Db 256 NMVPPPR 261

RESULT 20
S18456
tubulin beta chain (clone 16T) - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S18456
R;Ahmad, S.; Singh, B.; Gupta, R.S.
Biochim. Biophys. Acta 1090, 252-254, 1991
A;Title: Nucleotide sequences of three different isoforms of beta-tubulin cDNA from Chinese hamster ovary cells
A;Reference number: S18456; MUID:92031702; PMID:1657186
A;Accession: S18456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-444 <AHM>
A;Cross-references: UNIPROT:Q60454; EMBL:X60784; NID:G49480; PIDN:CAA43197.1; PID:G49481
C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPPR 7
|||||
Db 256 NMVPPPR 262

RESULT 21
E25437
tubulin beta-5 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 09-Jul-2004
C;Accession: E25437; S29017; S48745
R;Wang, D.; Villalante, A.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 103, 1903-1910, 1986
A;Title: The mammalian beta-tubulin repertoire: hematopoietic expression of a novel, hetero-oligomeric isoform
A;Reference number: A92746; MUID:87057644; PMID:3782288
A;Accession: E25437
A;Molecule type: mRNA
A;Residues: 1-444 <WAN>
A;Cross-references: UNIPROT:P05218; GB:X04663; NID:G55047; PIDN:CAA28369.1; PID:G55048
R;Lewis, S.A.; Lee, M.G.S.; Cowan, N.J.
J. Cell Biol. 101, 852-861, 1985
A;Title: Five mouse tubulin isoforms and their regulated expression during development.
A;Reference number: S29013; MUID:85289512; PMID:3839797
A;Accession: S29017

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 325-399, 'A', 401-444 <LEW>
A:Cross-references: EMBL:M28732; NID:g202230; PIDN:AAA40510.1; PID:g202231
A>Note: the authors translated the codon GCT for residue 400 as Gly
R:Mary, J.; Redeker, V.; le Caer, J.P.; Prome, J.C.; Rossier, J.
FEBS Lett. 353, 89-94, 1994
A>Title: Class I and Iva beta-tubulin isotypes expressed in adult mouse brain are glutamylated
A:Reference number: S48741; MUID:95010772; PMID:7926030
A:Accession: S48745
A>Status: preliminary
A:Molecule type: protein
A:Residues: 433-444 <MAR>
C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
|||||
Db 256 NMVPPFR 262

RESULT 22
S35191
tubulin beta-1 chain - fungus (Trichoderma viride)
C:Species: Trichoderma viride
C:Date: 13-Jan-1995 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S35191; S25553
R:Goldman, G.H.; Temmerman, W.; Jacobs, D.; Contreras, R.; van Montagu, M.; Herrera-Estrella, R.
Mol. Gen. Genet. 240, 73-80, 1993
A>Title: A nucleotide substitution in one of the beta-tubulin genes of Trichoderma viride
A:Reference number: S35191; MUID:93341462; PMID:8341264
A:Accession: S35191
A:Molecule type: DNA
A:Residues: 1-444 <GOL>
A:Cross-references: UNIPROT:P31864; EMBL:Z15054
R:Goldman, G.G.H.; Temmerman, W.W.; Herrera-Estrella, A.A.; Jacobs, D.D.; Contreras, R.R.
submitted to the EMBL Data Library, July 1992
A:Description: A nucleotide substitution in one of the beta-tubulin genes of Trichoderma viride
A:Reference number: S25553
A:Accession: S25553
A:Molecule type: DNA
A:Residues: 1-5, 'SV', 6-31, 'SS', 32-47, 50-444 <GOW>
A:Cross-references: EMBL:Z15054; NID:g5204; PIDN:CAA78764.1; PID:g5205
C:Genetics:
A:Gene: tub1
A:Introns: 4/3; 12/3; 21/3; 53/3
C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
|||||
Db 256 NMVPPFR 262

RESULT 23
UBCHB
tubulin beta chain, embryonic - chicken
N:Alternate names: tubulin beta-2
C:Species: Gallus gallus (chicken)
C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C:Accession: A02974; S29136
R:Valenzuela, P.; Quiroga, M.; Zaldivar, J.; Rutter, W.J.; Kirschner, M.W.; Cleveland, D.
Nature 289, 650-655, 1981
A>Title: Nucleotide and corresponding amino acid sequences encoded by alpha and beta tubulin genes
A:Reference number: A93246; MUID:81123093; PMID:7464932
A:Accession: A02974
A:Molecule type: mRNA

A:Residues: 1-445 <VAL>
A:Cross-references: UNIPROT:P32882; GB:J00913; NID:g212839; PIDN:AAA49123.1; PID:g212840
R:Sullivan, K.F.; Lau, J.T.Y.; Cleveland, D.W.
Mol. Cell. Biol. 5, 2454-2465, 1985
A>Title: Apparent gene conversion between beta-tubulin genes yields multiple regulatory I
A:Reference number: I50435; MUID:86284689; PMID:3837190
A:Accession: I50436
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-445 <SUL>
A:Cross-references: GB:M11443; NID:g212843; PIDN:AAA49125.1; PID:g212844
C:Superfamily: tubulin
C:Keywords: microtubule
F:140-146/Region: tubulin/FtsZ GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif

Query Match 100.0%; Score 40; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
|||||
Db 256 NMVPPFR 262

RESULT 24
UBPGB
tubulin beta chain - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C:Accession: A02973; A31984; S29192
R:Kraus, E.; Little, M.; Kempf, T.; Hofer-Warbinek, R.; Ade, W.; Ponstingl, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 4156-4160, 1981
A>Title: Complete amino acid sequence of beta-tubulin from porcine brain.
A:Reference number: A93878; MUID:82037798; PMID:6945576
A:Accession: A02973
A:Molecule type: protein
A:Residues: 1-445 <KRA>
A:Cross-references: UNIPROT:P02554
A>Note: pig brain contains at least two forms of this protein; a peptide corresponding to

R:Zabrecky, J.R.; Cole, R.D.
Arch. Biochem. Biophys. 225, 475-481, 1983
A>Title: Localization of the ATP binding site on alpha-tubulin.
A:Reference number: A90072; MUID:8402547; PMID:6686710
A:Contents: annotation; guanine nucleotide binding sites
R:Hesse, J.; Thieraut, M.; Ponstingl, H.
J. Biol. Chem. 262, 15472-15475, 1987
A>Title: Tubulin sequence region beta155-174 is involved in binding exchangeable guanosi
A:Reference number: A58110; MUID:88058878; PMID:3680207
A:Contents: annotation; exchangeable guanine nucleotide binding site
A>Note: photoaffinity labelling and antibodies to synthetic peptides demonstrated the cor
ors suggest that region 63-77 may bind to the purine moiety, 155-174 to the ribose, while
R:Linsse, K.; Mandelkow, E.M.
J. Biol. Chem. 263, 15205-15210, 1988
A>Title: The GTP-binding peptide of beta-tubulin. Localization by direct photoaffinity la
A:Reference number: A31984; MUID:89008408; PMID:3170578
A:Accession: A31984
A:Molecule type: protein
A:Residues: 63-77 <LIN>
R:Ruediger, M.; Plessman, U.; Kloeppel, K.D.; Wehland, J.; Weber, K.
FEBS Lett. 308, 101-105, 1992
A>Title: Class II tubulin, the major brain beta tubulin isotype is polyglutamylated on gl
A:Reference number: S29191; MUID:92354756; PMID:1379548
A:Accession: S29192
A:Molecule type: protein
A:Residues: 1-11, 'X', 13-15, 154-162; 216-225; 434-439, 'EG', 442-444 <RUE>
A>Note: 7-leu was also found
C:Comment: Tubulin is found in the microtubules of eukaryote cells. It binds ATP on its c
fied.
C:Comment: The highly acidic carboxyl-terminal region may bind cations such as calcium.
C:Complex: heterodimer of alpha (see PIR:UBPGA) and beta chains
C:Superfamily: tubulin
C:Keywords: GTP binding; heterodimer; microtubule

F:63-77,137-146,155-174/Region: exchangeable (E) GTP binding site
 F:140-146/Region: tubulin/Ftez GTP/GDP-binding (G-G-T-G-(ST)-G) motif
 F:435/Binding site: polyglutamate (Glu) (covalent) #status experimental

-Query Match 100.0%; Score 40; DB 1; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 |||||
 Db 256 NMVPPFR 262

RESULT 25

A25113
 tubulin beta chain 15 - rat
 N:Alternate names: beta-tubulin (T beta-15)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 08-Dec-1994
 C:Accession: A25113
 R:Ginzburg, I.; Teichman, A.; Dodemont, H.J.; Behar, L.; Littauer, U.Z.
 EMBO J. 4, 3667-3673, 1985
 A:Title: Regulation of three beta-tubulin mRNAs during rat brain development.
 A:Reference number: A25113; MUID:86136010; PMID:2868892

A:Accession: A25113
 A:Molecule type: protein
 A:Residues: 1-445 <GIN>
 C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 |||||
 Db 256 NMVPPFR 262

RESULT 26

B45794
 tubulin beta chain - Ajellomyces capsulata
 C:Species: Ajellomyces capsulata, Histoplasma capsulatum
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
 C:Accession: B45794
 R:Harris, G.S.; Keath, E.J.; Medoff, J.
 J. Gen. Microbiol. 135, 1817-1832, 1989
 A:Title: Characterization of alpha and beta tubulin genes in the dimorphic fungus Histoplasma capsulatum
 A:Reference number: A45794; MUID:90132587; PMID:2614394

A:Accession: B45794
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-445 <HAR>
 A:Cross-references: GB:M28359
 C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 |||||
 Db 257 NMVPPFR 263

RESULT 27

A24701
 tubulin beta-3 chain - chicken
 C:Species: Gallus gallus (Chicken)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A24701; A27554
 R:Sullivan, K.F.; Machlin, P.S.; Ratnie III, H.; Cleveland, D.W.
 J. Biol. Chem. 261, 13317-13322, 1986
 A:Title: Sequence and expression of the chicken beta-3-tubulin gene. A vertebrate testis

A:Reference number: A24701; MUID:87008546; PMID:3759966

A:Accession: A24701

A:Molecule type: DNA

A:Residues: 1-445 <SUL>
 A:Cross-references: UNIPROT:P09206; GB:M14228; NID:g212829; PIDN:AAA49118.1; PID:g212830
 R:Sullivan, K.F.; Cleveland, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 83, 4327-4331, 1986

A:Title: Identification of conserved isotype-defining variable region sequences for four
 A:Reference number: A27554; MUID:86233423; PMID:3459176

A:Accession: A27554

A:Molecule type: DNA

A:Residues: 1-27, 'R', '29-81', 'GR', '84-306', 'D', '308-444', 'F' <SU2>

A:Cross-references: EMBL:M11443

C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 |||||
 Db 256 NMVPPFR 262

RESULT 28

I50435
 beta-1 tubulin - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I50435
 R:Sullivan, K.F.; Lau, J.T.Y.; Cleveland, D.W.
 Mol. Cell. Biol. 5, 2454-2465, 1985

A:Title: Apparent gene conversion between beta-tubulin genes yields multiple regulatory I

A:Reference number: I50435; MUID:86284689; PMID:3837190

A:Accession: I50435

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-445 <SUL>

A:Cross-references: UNIPROT:P09203; GB:M11442; NID:g212841; PIDN:AAA49124.1; PID:g212842

C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 |||||
 Db 256 NMVPPFR 262

RESULT 29

I38370
 beta-tubulin - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I38370
 R:Lewis, S.A.; Gilmarin, M.E.; Hall, J.L.; Cowan, N.J.
 J. Mol. Biol. 182, 11-20, 1985

A:Title: Three expressed sequences within the human beta-tubulin multigene family each d

A:Reference number: I38370; MUID:85210890; PMID:3999141

A:Accession: I38370

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-445 <RES>

A:Cross-references: UNIPROT:P05217; EMBL:X02344; NID:g37493; PIDN:CAA26203.1; PID:g37494

C:Genetics: 19/3; 56/1; 93/1

C:Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

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Qy      1 NMVPPFR 7
      |||||
Db      256 NMVPPFR 262

RESULT 30
T08726
tubulin beta chain - human
N:Alternate names: hypothetical protein DKFZp566f223.1
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T08726; S45140
R:Koshner, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16473
A:Accession: T08726
A:Molecule type: mRNA
A:Residues: 121-445 <KOE>
A:Cross-references: UNIPROT:Q9UGA2; UNIPROT:Q13885; EMBL:AL050056
A:Experimental source: fetal kidney; clone DKFZp566f223
R:Jeffers, H.; Wiemann, S.; Ansoorge, W.
submitted to the EMBL Data Library, June 1994
A:Description: Cloning and vaccinia virus expression of a cDNA containing the complete c
A:Reference number: S45141
A:Accession: S45140
A:Molecule type: mRNA
A:Residues: 1-200, 'S', 202-386, 'A', 388-445 <LEF>
A:Cross-references: EMBL:X79535; NID:G496886; PID:G496887
C:Comment: Tubulin is found in the microtubules of all eukaryote cells. It binds ATP on
ied.
C:Comment: The highly acidic carboxyl-terminal region may bind cations such as calcium.
C:Genetics:
A:Note: DKFZp566f223.1
C:Complex: polymerized heterodimer; heterodimer of alpha and beta chains
C:Complex: heterodimer; alpha and beta chain
C:Superfamily: tubulin
C:Keywords: GTP binding; heterodimer

Query Match      100.0%; Score 40; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 NMVPPFR 7
      |||||
Db      256 NMVPPFR 262

RESULT 31
S37144
tubulin beta chain - winter flounder
C:Species: Pseudopleuronectes americanus (winter flounder)
C:Date: 25-Dec-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S37144
R:Watson, C.E.; Yoshida, E.N.; Davies, P.L.
submitted to the EMBL Data Library, August 1993
A:Description: The predicted amino acid sequence of a testis B-tubulin from winter flou.
A:Reference number: S37144
A:Accession: S37144
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-445 <WAT>
A:Cross-references: UNIPROT:Q91240; EMBL:X74492; NID:G400422; PID:CAAS2604.1; PID:G4004
C:Superfamily: tubulin

Query Match      100.0%; Score 40; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 NMVPPFR 7
      |||||
Db      256 NMVPPFR 262

```

```

RESULT 32
C25437
tubulin beta-3 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 09-Jul-2004
C:Accession: C25437; S48743
R:Wang, D.; Villasanté, A.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 103, 1903-1910, 1986
A:Title: The mammalian beta-tubulin repertoire: hematopoietic expression of a novel, heter
A:Reference number: A92746; MUID:87057644; PMID:3782288
A:Accession: C25437
A:Molecule type: mRNA
A:Residues: 1-445 <WAN>
A:Cross-references: UNIPROT:P05217
R:Mary, J.; Redeker, V.; le Caer, J.P.; Prone, J.C.; Rossier, J.
FEBS Lett. 353, 89-94, 1994
A:Title: Class I and IVA beta-tubulin isotypes expressed in adult mouse brain are glutamy
A:Reference number: S48741; MUID:95010772; PMID:7926030
A:Accession: S48743
A:Status: preliminary
A:Molecule type: protein
A:Residues: 427-445 <MAR>
C:Superfamily: tubulin

Query Match      100.0%; Score 40; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 NMVPPFR 7
      |||||
Db      256 NMVPPFR 262

RESULT 33
JC7788
beta-tubulin - basidiomycete (Pleurotus sajor-caju)
N:Alternate names: tubulin 1
C:Species: Pleurotus sajor-caju
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
R:Kim, B.G.; Yoo, Y.B.; Kwon, S.T.; Magae, Y.
Biosci. Biotechnol. Biochem. 65, 2280-2283, 2001
A:Title: Molecular characterization of beta-tubulin gene from Pleurotus sajor-caju.
A:Reference number: JC7788
A:Accession: JC7788
A:Molecule type: DNA
A:Residues: 1-445 <KIM>
A:Cross-references: UNIPROT:Q9UWF3; GB:AF132911
C:Genetics:
A:Gene: tubl
A:Introns: 11/3; 17/1; 105/1; 132/1; 181/3; 258/1; 311/3; 406/3; 428/2
C:Superfamily: tubulin

Query Match      100.0%; Score 40; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 NMVPPFR 7
      |||||
Db      256 NMVPPFR 262

RESULT 34
A27810
tubulin beta-2 chain - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jun-2002
C:Accession: A27810
R:Rudolph, J.E.; Kimble, M.; Hoyle, H.D.; Subler, M.A.; Raff, E.C.
Mol. Cell. Biol. 7, 2231-2242, 1987
A:Title: Three Drosophila beta-tubulin sequences: a developmentally regulated isoform (be
A:Reference number: A93092; MUID:87257938; PMID:3037352

```

```
A:Accession: A27810
A:Molecule type: DNA
A:Residues: 1-446 <RUD>
A:Cross-references: GB:M16922; NID:g158740; PIDN:AAA28990.1; PID:g159741
A>Note: in GenBank entry DROTUBB2, release 109, the source is designated as Drosophila e
C:Genetics:
A:Gene: FlyBase:beta-Tub85D
A:Cross-references: FlyBase:FBgn0003889
A:Introns: 19/3; 56/1; 131/3
C:Superfamily: tubulin

Query Match      100.0%; Score 40; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 35
B27554
tubulin beta-5 chain - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: B27554; A25401
R:Sullivan, K.F.; Cleveland, D.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 4327-4331, 1986
A:Title: Identification of conserved isotype-defining variable region sequences for four
A:Reference number: A27554; MUID:86233423; PMID:3459176
A:Accession: B27554
A:Molecule type: DNA
A:Residues: 1-446 <SUL>
A:Cross-references: UNIPROT:P09653; EMBL:M11443
R:Sullivan, K.F.; Havercroft, J.C.; Machlin, P.S.; Cleveland, D.W.
Mol. Cell. Biol. 6, 4409-4416, 1986
A:Title: Sequence and expression of the chicken beta-5- and beta-4-tubulin genes define
A:Reference number: A25401; MUID:87089799; PMID:3025656
A:Accession: A25401
A:Molecule type: DNA
A:Residues: 1-82, 'OL', 85-238, 'SL', 241-306, 'H', 308-433, 'E', 435-446 <SU2>
A:Cross-references: GB:L29435; GB:M14683; GB:N00047; NID:G459712; PIDN:AAA49126.1; PID:G
C:Superfamily: tubulin

Query Match      100.0%; Score 40; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262

RESULT 36
A27424
tubulin beta chain - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27424
R:Murphy, D.B.; Wallis, K.T.; Machlin, P.S.; Ratnie III, H.; Cleveland, D.W.
J. Biol. Chem. 262, 14305-14312, 1987
A:Title: The sequence and expression of the divergent beta-tubulin in chicken erythrocyt
A:Reference number: A27424; MUID:88007687; PMID:2888766
A:Accession: A27424
A:Molecule type: mRNA
A:Residues: 1-446 <MUR>
A:Cross-references: UNIPROT:P09207; GB:J02828; NID:g212833; PIDN:AAA49120.1; PID:g212834
C:Superfamily: tubulin
C:Keywords: microtubule

Query Match      100.0%; Score 40; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262
```

RESULT 37

```
S08403
tubulin beta chain - grass mildew
C:Species: Erysiphe graminis f. sp. hordei (grass mildew)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S08403
R:Sherwood, J.E.; Somerville, S.C.
Nucleic Acids Res. 18, 1052, 1990
A:Title: Sequence of the Erysiphe graminis f. sp. hordei gene encoding beta-tubulin.
A:Reference number: S08403; MUID:90192093; PMID:2315020
A:Accession: S08403
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-446 <SHE>
A:Cross-references: UNIPROT:P16040; EMBL:X51326; NID:g2697; PIDN:CAA35709.1; PID:g2698
C:Genetics:
A:Introns: 4/3; 12/3; 21/1; 35/2; 53/3; 317/2
C:Superfamily: tubulin

Query Match      100.0%; Score 40; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262
```

RESULT 38

```
A48407
neural class-II beta tubulin, Ncn beta 1 - black rockcod
C:Species: Notothenia coriiceps (black rockcod)
C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48407
R:Detrich III, H.W.; Parker, S.K.
Cell Motil. Cytoskeleton 24, 156-166, 1993
A:Title: Divergent neural beta tubulin from the Antarctic fish Notothenia coriiceps negle
A:Reference number: A48407; MUID:93223253; PMID:8467523
A:Accession: A48407
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-446 <DET>
A:Cross-references: UNIPROT:P36221; GB:S57698; NID:g299442; PIDN:AAB26110.1; PID:g299443
A:Experimental source: subsp. neglecta
A>Note: sequence extracted from NCBI backbone (NCBI:129127, NCBIP:129128)
C:Superfamily: tubulin

Query Match      100.0%; Score 40; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 256 NMVPPFR 262
```

RESULT 39

```
S25554
tubulin beta chain - fungus (Trichoderma viride)
C:Species: Trichoderma viride
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S35192; S25554
R:Goldman, G.H.; Temmerman, W.; Jacobs, D.; Contreras, R.; van Montagu, M.; Herrera-Batre
Mol. Gen. Genet. 240, 73-80, 1993
A:Title: A nucleotide substitution in one of the beta-tubulin genes of Trichoderma viride
A:Reference number: S35191; MUID:93341462; PMID:8341264
A:Accession: S35192
```

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-446 <GOL>
 A;Cross-references: UNIPROT:P31863; EMBL:Z15055; NID:G5206; PIDN:CAA78765.1; PID:G5207
 C;Genetics:
 A;Introns: 4/3; 12/3; 53/3; 317/2
 C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 446;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 |||||
 Db 256 NMVPPFR 262

RESULT 40
 S49328
 tubulin beta-2 chain - Erysiphe pisi
 C;Species: Erysiphe pisi
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Jul-1997
 C;Accession: S49328
 R;Cannell, M.E.; Green, J.R.; Callow, J.C.
 submitted to the EMBL Data Library, September 1994
 A;Description: A method for the production of a conventional cDNA library containing pea
 A;Reference number: S49328
 A;Accession: S49328
 A;Molecule type: mRNA
 A;Residues: 1-447 <CAN>
 A;Cross-references: EMBL:X81961
 C;Genetics:
 A;Gene: tub2
 C;Superfamily: tubulin

Query Match 100.0%; Score 40; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 |||||
 Db 256 NMVPPFR 262

Search completed: July 20, 2005, 17:32:24
 Job time : 12.1852 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 17:19:48 ; Search time 59.6296 Seconds
(without alignments)
60.114 Million cell updates/sec

Title: US-10-766-480A-1
Perfect score: 40
Sequence: 1 NMVPPFR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	79	2 Q8J1D8	Q8J1D8 cetraria ol
2	40	100.0	83	2 Q8J1D3	Q8J1D3 nephromopsi
3	40	100.0	84	2 Q8J1C1	Q8J1C1 cetraria co
4	40	100.0	84	2 Q87605	Q87605 neofuscelia
5	40	100.0	85	2 Q87608	Q87608 platismatia
6	40	100.0	86	2 Q8NKC6	Q8NKC6 glomus moss
7	40	100.0	87	2 P78635	P78635 fusarium dl
8	40	100.0	87	2 P79986	P79986 fusarium sp
9	40	100.0	89	2 P78681	P78681 fusarium sp
10	40	100.0	92	2 O74605	O74605 fusarium be
11	40	100.0	92	2 O74611	O74611 fusarium co
12	40	100.0	93	2 P78631	P78631 fusarium bu
13	40	100.0	93	2 P78644	P78644 fusarium in
14	40	100.0	93	2 P78650	P78650 fusarium na
15	40	100.0	93	2 P78657	P78657 fusarium ox
16	40	100.0	93	2 P87101	P87101 fusarium ps
17	40	100.0	93	2 Q6J1T4	Q6J1T4 gibberella
18	40	100.0	94	2 Q8J1J1	Q8J1J1 fusarium sp
19	40	100.0	95	2 Q6J1S9	Q6J1S9 fusarium br
20	40	100.0	95	2 Q6J1T1	Q6J1T1 fusarium co
21	40	100.0	96	2 O74619	O74619 fusarium sp
22	40	100.0	96	2 Q6J1T5	Q6J1T5 gibberella
23	40	100.0	96	2 Q9CON6	Q9CON6 fusarium su
24	40	100.0	96	2 Q8J1J0	Q8J1J0 fusarium su
25	40	100.0	97	2 O74606	O74606 fusarium be
26	40	100.0	97	2 P78678	P78678 gibberella
27	40	100.0	97	2 Q6J1T3	Q6J1T3 fusarium sp
28	40	100.0	97	2 Q9HDG4	Q9HDG4 gibberella
29	40	100.0	97	2 Q9HDG5	Q9HDG5 fusarium cu
30	40	100.0	97	2 Q9HDG6	Q9HDG6 fusarium ce
31	40	100.0	97	2 Q9HDG7	Q9HDG7 fusarium ps

32	40	100.0	97	2 Q9P4G7	Q9P4G7 fusarium sp
33	40	100.0	98	2 O09197	O09197 fusarium re
34	40	100.0	98	2 O74603	O74603 fusarium an
35	40	100.0	98	2 O74604	O74604 fusarium an
36	40	100.0	98	2 O74607	O74607 fusarium br
37	40	100.0	98	2 O74608	O74608 fusarium bu
38	40	100.0	98	2 O74609	O74609 gibberella
39	40	100.0	98	2 O74610	O74610 fusarium co
40	40	100.0	98	2 O74612	O74612 fusarium de
41	40	100.0	98	2 O74613	O74613 fusarium la
42	40	100.0	98	2 O74614	O74614 fusarium sa
43	40	100.0	98	2 O74615	O74615 fusarium ps
44	40	100.0	98	2 O74616	O74616 fusarium ra
45	40	100.0	98	2 O74617	O74617 fusarium ni

ALIGNMENTS

RESULT 1					
Q8J1D8	Q8J1D8	PRELIMINARY;	PRT;	79 AA.	
AC	Q8J1D8;	2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)			
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)			
DE	Beta-tubulin (Fragment).				
OS	Cetraria olivetorum.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;				
OC	Lecanorales; Lecanorineae; Parmeliaceae; Cetraria.				
OX	NCBI_TaxID=180479;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Thell A., Stenroos S., Feuerer T., Kaernefelt I., Myllys L.,				
RA	Hyonenen J.;				
RT	"Phylogeny of cetrarioid lichens (Parmeliaceae) inferred from ITS and				
RT	beta-tubulin sequences, morphology, anatomy, and secondary				
RT	chemistry."				
RL	Mycol. Prog. 1:235-254(2002).				
DR	EMBL: AF449716; AAN76781.1; -				
DR	GO; GO:0045298; C:tubulin; IEA.				
DR	GO; GO:0005255; F:GTP binding; IEA.				
DR	GO; GO:0003924; F:GTPase activity; IEA.				
DR	GO; GO:0005198; F:structural molecule activity; IEA.				
DR	GO; GO:0046785; P:microtubule polymerization; IEA.				
DR	GO; GO:0007018; P:microtubule-based movement; IEA.				
DR	InterPro; IPR002453; Beta tubulin.				
DR	InterPro; IPR003008; Tubulin FtsZ.				
DR	InterPro; IPR008280; Tub FtsZ C.				
DR	Pfam; PF00091; Tubulin; I.				
DR	Pfam; PF03953; Tubulin C; 1.				
DR	PRINTS; PR01163; BETA-TUBULIN.				
KW	GTP-binding.				
FT	NON TER 1				
FT	NON TER 79				
SQ	SEQUENCE 79 AA; 8756 MW; D1E1FD9EC973A28 CRC64;				
Query Match 100.0%; Score 40; DB 2; Length 79;					
Best Local Similarity 100.0%; Pred. No. 1.4;					
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 NMVPPFR 7				
Db	51 NMVPPFR 57				
RESULT 2					
Q8J1D3	Q8J1D3	PRELIMINARY;	PRT;	83 AA.	
AC	Q8J1D3;				
DT	01-MAR-2003	(TrEMBLrel. 23, Created)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)			
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)			

DE Beta-tubulin (Fragment).
OS Nephromopsis ornata
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
OC Lecanorales; Lecanorineae; Parmeliaceae; Nephromopsis.
OX NCBI_TaxID=180485;
RN [1]
RP SEQUENCE FROM N.A.
RA Thell A., Stenroos S., Feuerer T., Kaernefelt I., Myllys L.,
RA Hyvoenen J.;
RT "Phylogeny of cetrarioid lichens (Parmeliaceae) inferred from ITS and
RT beta-tubulin sequences, morphology, anatomy, and secondary
RT chemistry."
RL Mycol. Prog. 1:235-254(2002).
DR EMBL; AF449721; AAN76798.1; -;
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR InterPro; IPR008280; Tub_FtsZ_C.
DR Pfam; PF00091; Tubulin; I.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
KW GTP-binding.
FT NON TER 1 1
FT NON TER 83 83
SQ SEQUENCE 83 AA; 9183 MW; E280410A91E1F1D9 CRC64;
Query Match 100.0%; Score 40; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NMVFPFR 7
Db 51 NMVFPFR 57
RESULT 3
Q8J1C1 PRELIMINARY; PRT; 84 AA.
AC Q8J1C1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Cetraria commixta.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
OC Lecanorales; Lecanorineae; Parmeliaceae; Cetraria.
OX NCBI_TaxID=180473;
RN [1]
RP SEQUENCE FROM N.A.
RA Thell A., Stenroos S., Feuerer T., Kaernefelt I., Myllys L.,
RA Hyvoenen J.;
RT "Phylogeny of cetrarioid lichens (Parmeliaceae) inferred from ITS and
RT beta-tubulin sequences, morphology, anatomy, and secondary
RT chemistry."
RL Mycol. Prog. 1:235-254(2002).
DR EMBL; AF449735; AAN76798.1; -;
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR InterPro; IPR008280; Tubulin; I.
DR Pfam; PF00091; Tubulin; I.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.

KW GTP-binding.
FT NON TER 1 1
FT NON TER 84 84
SQ SEQUENCE 84 AA; 9209 MW; A8E2F69CD0D5B5F5 CRC64;
Query Match 100.0%; Score 40; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NMVFPFR 7
Db 51 NMVFPFR 57
RESULT 4
Q876Q5 PRELIMINARY; PRT; 84 AA.
AC Q876Q5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-tubulin (Fragment).
OS Neofuscelia pulla.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
OC Lecanorales; Lecanorineae; Parmeliaceae; Neofuscelia.
OX NCBI_TaxID=172823;
RN [1]
RP SEQUENCE FROM N.A.
RA Thell A., Stenroos S., Feuerer T., Kaernefelt I., Myllys L.,
RA Hyvoenen J.;
RT "Phylogeny of cetrarioid lichens (Parmeliaceae) inferred from ITS and
RT beta-tubulin sequences, morphology, anatomy, and secondary
RT chemistry."
RL Mycol. Prog. 1:235-254(2002).
DR EMBL; AF457928; AAO38202.1; -;
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR InterPro; IPR008280; Tub_FtsZ_C.
DR Pfam; PF00091; Tubulin; I.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
KW GTP-binding.
FT NON TER 1 1
FT NON TER 84 84
SQ SEQUENCE 84 AA; 9326 MW; 356E1F540A91E1E6 CRC64;
Query Match 100.0%; Score 40; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NMVFPFR 7
Db 51 NMVFPFR 57
RESULT 5
Q876Q8 PRELIMINARY; PRT; 85 AA.
AC Q876Q8
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-tubulin (Fragment).
OS Platismatia glauca.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Lecanoromycetes;
OC Lecanorales; Lecanorineae; Parmeliaceae; Platismatia.
OX NCBI_TaxID=78070;

RN SEQUENCE FROM N.A.
 RP Thell A., Stenroos S., Feuerer T., Kaernefelt I., Myllys L.,
 RA Hyvoenen J.;
 RT "Phylogeny of cetrarioid lichens (Parmeliaceae) inferred from ITS and
 RT beta-tubulin sequences, morphology, anatomy, and secondary
 RT chemistry";
 RL Mycol. Prog. 1:235-254 (2002).
 DR EMBL; AF457925; AAC38200.1; -.
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR003008; Tubulin_FtsZ.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF00091; Tubulin; I.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 KW GTP-binding. 1 1
 FT NON_TER 85 85
 FT NON_TER 85 85
 SQ SEQUENCE 85 AA; 9414 MW; BBB9A0E7EA8D6E27 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
 DB 54 NMVPPFR 60

RESULT 6
 Q8NKC6 PRELIMINARY; PRT; 86 AA.
 ID AC Q8NKC6
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative beta-tubulin (Fragment).
 GN Names:btub2;
 OS Glomus mossae.
 OC Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
 OC Glomeraceae; Glomus.
 OX NCBI_TaxID=27381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22719885; PubMed=12836081;
 RA Rhody D., Stommel M., Roeder C., Mann P., Franken P.;
 RT "Differential RNA accumulation of two g-tubulin genes in arbuscular
 RT mycorrhizal fungi";
 RL Mycorrhiza 13:137-142(2003).
 DR EMBL; AJ459248; CAD30554.1; -.
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR003008; Tubulin_FtsZ.
 DR Pfam; PF00091; Tubulin; 1.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 KW GTP-binding. 1 1
 FT NON_TER 86 86
 FT NON_TER 86 86
 SQ SEQUENCE 86 AA; 9694 MW; 4C5CDC316F9E8C3 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
 DB 71 NMVPPFR 77

RESULT 7
 P78635 PRELIMINARY; PRT; 87 AA.
 ID AC P78635; P87094;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium dlamini.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OX NCBI_TaxID=42669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=NRRL 13164;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpsv.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
 RT lineage of the fungus Fusarium are nonorthologous";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=NRRL 13164;
 RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
 RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
 RT species complex";
 RL Mycologia 90:465-493(1998).
 DR EMBL; U34485; AAC26335.1; -.
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 FT NON_TER 1 1
 FT NON_TER 87 87
 SQ SEQUENCE 87 AA; 9982 MW; D7207CFD47D56032 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
 DB 8 NMVPPFR 14

RESULT 8
 P97986 PRELIMINARY; PRT; 87 AA.
 ID AC P97986
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium sp. NRRL22903.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 OC Fusarium oxysporum complex.

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OX NCBI_TaxID=56677;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 22903;
RA MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpsv.1996.0376;
RX O'Donnell K., Cigelnik E.;
RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
lineage of the fungus Fusarium are nonorthologous.";
RL Mol. Phylogenet. Evol. 7:103-116(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 22903;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex.";
RL Mycologia 90:465-493(1998).
DR EMBL; U34480; AAC26367.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
FT NON_TER 87
SQ SEQUENCE 87 AA; 9955 MW; C6D07CFD47D56032 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
DB 8 NMVPPFR 14

RESULT 9
P78681 PRELIMINARY; PRT; 89 AA.
AC P78681;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium sp. NRRL 20459.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56675;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 20459;
RA O'Donnell K., Cigelnik E.;
RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
lineage of the fungus Fusarium are nonorthologous.";
RL Mol. Phylogenet. Evol. 7:103-116(1997).
DR EMBL; U34496; AAB58455.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR Pfam; PF03953; Tubulin_C; 1.
DR NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10234 MW; 0520521331BC7B79 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
DB 8 NMVPPFR 14

RESULT 10
O74605 PRELIMINARY; PRT; 92 AA.
AC O74605;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium begoniae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
OC Gibberella fujikuroi complex.
OX NCBI_TaxID=48487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25300;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex.";
RL Mycologia 90:465-493(1998).
DR EMBL; U61621; AAC26456.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
FT NON_TER 92
SQ SEQUENCE 92 AA; 10534 MW; E8DD1D9B6DF6D07C CRC64;

Query Match 100.0%; Score 40; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
DB 8 NMVPPFR 14

RESULT 11
O74611 PRELIMINARY; PRT; 92 AA.
AC O74611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium concolor.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=48492;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL13994;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex.";
RL Mycologia 90:465-493(1998).
DR EMBL; U61627; AAC26462.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
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OX NCBI_TaxID=56677;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 22903;
RA MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpsv.1996.0376;
RX O'Donnell K., Cigelnik E.;
RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
lineage of the fungus Fusarium are nonorthologous.";
RL Mol. Phylogenet. Evol. 7:103-116(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 22903;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex.";
RL Mycologia 90:465-493(1998).
DR EMBL; U34480; AAC26367.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
FT NON_TER 87
SQ SEQUENCE 87 AA; 9955 MW; C6D07CFD47D56032 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
DB 8 NMVPPFR 14

RESULT 9
P78681 PRELIMINARY; PRT; 89 AA.
AC P78681;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium sp. NRRL 20459.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56675;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 20459;
RA O'Donnell K., Cigelnik E.;
RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
lineage of the fungus Fusarium are nonorthologous.";
RL Mol. Phylogenet. Evol. 7:103-116(1997).
DR EMBL; U34496; AAB58455.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR Pfam; PF03953; Tubulin_C; 1.
DR NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10234 MW; 0520521331BC7B79 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
DB 8 NMVPPFR 14

RESULT 10
O74605 PRELIMINARY; PRT; 92 AA.
AC O74605;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium begoniae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
OC Gibberella fujikuroi complex.
OX NCBI_TaxID=48487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25300;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex.";
RL Mycologia 90:465-493(1998).
DR EMBL; U61621; AAC26456.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
FT NON_TER 92
SQ SEQUENCE 92 AA; 10534 MW; E8DD1D9B6DF6D07C CRC64;

Query Match 100.0%; Score 40; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMVPPFR 7
DB 8 NMVPPFR 14

RESULT 11
O74611 PRELIMINARY; PRT; 92 AA.
AC O74611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium concolor.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=48492;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL13994;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex.";
RL Mycologia 90:465-493(1998).
DR EMBL; U61627; AAC26462.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
```


DR GO: GO:0003924; P:GTPase activity; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0046785; P:microtubule polymerization; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR002453; Beta tubulin.
 DR InterPro: IPR008280; Tub_FtsZ_C.
 DR Pfam: PF03953; Tubulin_C; 1.
 DR PRINTS: PRO1163; BETATUBULIN.
 FT NON_TER 1 92
 FT NON_TER 92 92
 SQ SEQUENCE 92 AA; 10561 MW; E8DD1D9E6DE7207C CRC64;

Query Match 100.0%; Score 40; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7
 Db 8 NMVPPPR 14

RESULT 12

ID P78631 PRELIMINARY; PRT; 93 AA.
 AC P78631
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium buharicum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxID=44411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 13371;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpev.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
 RT lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 DR EMBL; U34494; AAC58449.1; -.
 DR GO: GO:0045298; C:tubulin; IEA.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0003924; P:GTPase activity; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0046785; P:microtubule polymerization; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR002453; Beta tubulin.
 DR Pfam: PF03953; Tubulin_C; 1.
 DR PRINTS: PRO1163; BETATUBULIN.
 FT NON_TER 1 93
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10734 MW; 6218CC1CB8E6CE73C CRC64;

Query Match 100.0%; Score 40; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7
 Db 8 NMVPPPR 14

RESULT 13

ID P78644 PRELIMINARY; PRT; 93 AA.
 AC P78644
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium inflexum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 OX NCBI_TaxID=42671;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 20433;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpev.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
 RT lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 DR EMBL; U34483; AAC26345.1; -.

RESULT 14

ID P78650 PRELIMINARY; PRT; 93 AA.
 AC P78650
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium napiforme.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OX NCBI_TaxID=42672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 13604;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpev.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
 RT lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 DR EMBL; U34483; AAC26345.1; -.

RESULT 15

ID P78650 PRELIMINARY; PRT; 93 AA.
 AC P78650
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium napiforme.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OX NCBI_TaxID=42672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 13604;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpev.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
 RT lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 DR EMBL; U34483; AAC26345.1; -.

OS Fusarium inflexum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 OX NCBI_TaxID=42671;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 20433;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpev.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
 RT lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 DR EMBL; U34490; AAC26341.1; -.
 DR GO: GO:0045298; C:tubulin; IEA.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0003924; P:GTPase activity; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0046785; P:microtubule polymerization; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR002453; Beta tubulin.
 DR InterPro: IPR008280; Tub_FtsZ_C.
 DR Pfam: PF03953; Tubulin_C; 1.
 DR PRINTS: PRO1163; BETATUBULIN.
 FT NON_TER 1 93
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10708 MW; 2308DD1D9E6DE720 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7
 Db 8 NMVPPPR 14

DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 FT NON_TER 1 1
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10681 MW; 2308DD1D9E6DF6D0 CRC64;
 Query Match 100.0%; Score 40; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMVPPFR 7
 Db 8 NMVPPFR 14
 RESULT 15
 ID P78657 PRELIMINARY; PRT; 93 AA.
 AC P78657; P87098;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium;
 OC Fusarium oxysporum complex.
 RN NCBI_TaxID=5507;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 13307;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpcv.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0046785; P:structural molecule activity; IEA.
 DR GO; GO:0007018; P:microtubule polymerization; IEA.
 DR InterPro; IPR002453; Beta tubulin.
 DR PRINTS; PR01163; BETATUBULIN.
 FT NON_TER 1 1
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10708 MW; 2308DD1D9E6DE720 CRC64;
 Query Match 100.0%; Score 40; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMVPPFR 7
 Db 8 NMVPPFR 14
 RESULT 16
 ID P87101 PRELIMINARY; PRT; 93 AA.
 AC P87101
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium pseudocircinatum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 RN NCBI_TaxID=56676;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 22946;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpcv.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0046785; P:structural molecule activity; IEA.
 DR GO; GO:0007018; P:microtubule polymerization; IEA.
 DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 FT NON_TER 1 1
 FT NON_TER 93 93
 SQ SEQUENCE 93 AA; 10681 MW; 2308DD1D9E6DF6D0 CRC64;
 Query Match 100.0%; Score 40; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMVPPFR 7
 Db 8 NMVPPFR 14
 RESULT 17
 ID Q6JIT4 PRELIMINARY; PRT; 93 AA.
 AC Q6JIT4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Gibberella zeae (Fusarium graminearum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 RN NCBI_TaxID=5518;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL34079;
 RX PubMed=15121083; DOI=10.1016/j.fgb.2004.03.003;
 RA O'Donnell K., Ward T.J., Geiser D.M., Corby Kistler H., Aoki T.;
 RT "Genealogical concordance between the mating type locus and seven other nuclear genes supports formal recognition of nine phylogenetically distinct species within the Fusarium graminearum clade.";
 RL Fungal Genet. Biol. 41:600-623(2004).
 DR EMBL; AY452950; AAR45991.1; -.
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.

DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PRO1163; BETATUBULIN.

FT NON TER 1
 FT NON TER 93
 SQ SEQUENCE 93 AA; 10738 MW; 23F9F524E43E522C CRC64;

Query Match 100.0%; Score 40; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 1 NMVPPFR 7

RESULT 18

Q9URJ1 PRELIMINARY; PRT; 94 AA.

AC Q9URJ1, 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium sp. NRRL 25309.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OC NCBI_TaxID=122382;

Qy 1 NMVPPFR 7
 Db 1 NMVPPFR 7

Query Match 100.0%; Score 40; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 8 NMVPPFR 14

RESULT 19

Q6JIS9 PRELIMINARY; PRT; 95 AA.

AC Q6JIS9, 2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium brasilicum.

Query Match 100.0%; Score 40; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 8 NMVPPFR 14

RESULT 20

Q6JIT1 PRELIMINARY; PRT; 95 AA.

AC Q6JIT1, 2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium brasilicum.

Qy 1 NMVPPFR 7
 Db 5 NMVPPFR 11

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OC NCBI_TaxID=281087;

DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PRO1163; BETATUBULIN.

FT NON TER 1
 FT NON TER 95
 SQ SEQUENCE 95 AA; 10922 MW; F17735BB673697CC CRC64;

Query Match 100.0%; Score 40; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 5 NMVPPFR 11

RESULT 20

Q6JIT1 PRELIMINARY; PRT; 95 AA.

AC Q6JIT1, 2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium cortaderiae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OC NCBI_TaxID=281068;

Qy 1 NMVPPFR 7
 Db 5 NMVPPFR 11

Query Match 100.0%; Score 40; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 5 NMVPPFR 11

Query Match 100.0%; Score 40; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 5 NMVPPFR 11

Query Match 100.0%; Score 40; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 5 NMVPPFR 11

Query Match 100.0%; Score 40; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

Qy 1 NMVPPFR 7
 Db 5 NMVPPFR 11

Query Match 100.0%; Score 40; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

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FT  NON_TER      1      1
FT  NON_TER      95     95
SQ  SEQUENCE     95 AA; 10922 MW;  F17735BB6736970C CRC64;
      Query Match      100.0%; Score 40; DB 2; Length 95;
      Best Local Similarity 100.0%; Pred. No. 1.7;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 NMVPPFR 7
    |||||
Db  5 NMVPPFR 11

RESULT 21
O74619 ID O74619 PRELIMINARY; PRT; 96 AA.
AC O74619;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium sp. NRRL 25195.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=122394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25195;
RA O'Donnell K., Gigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
RT species complex.";
RL Mycologia 90:465-493 (1998).
DR EMBL; U61636; AAC26471.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta tubulin.
DR Pfam; PF031953; Tubulin_C_1_.
DR PRINTS; PR01163; BETATUBULIN.
FT NON_TER      1
FT NON_TER      96
SQ SEQUENCE     96 AA; 11074 MW;  B377DA897464F79B CRC64;

      Query Match      100.0%; Score 40; DB 2; Length 96;
      Best Local Similarity 100.0%; Pred. No. 1.7;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 NMVPPFR 7
    |||||
Db  6 NMVPPFR 12

RESULT 22
Q6JIT5 ID Q6JIT5 PRELIMINARY; PRT; 96 AA.
AC Q6JIT5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-tubulin (Fragment).
OS Gibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=5518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL31084;
RA O'Donnell K., Ward T.J., Geiser D.M., Corby Kistler H., Aoki T.;

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RT "Genealogical concordance between the mating type locus and seven
RT other nuclear genes supports formal recognition of nine
RT phylogenetically distinct species within the Fusarium graminearum
RT clade.";
RL Fungal Genet. Biol. 41:600-623 (2004).
DR EMBL; AY452949; AAT45990.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta tubulin.
DR InterPro; IPR008280; Tub_FtsZ_C.
DR Pfam; PF03953; Tubulin_C_1_.
DR PRINTS; PR01163; BETATUBULIN.
FT NON_TER      1
FT NON_TER      96
SQ SEQUENCE     96 AA; 11022 MW;  C6EDA414638B6166 CRC64;

      Query Match      100.0%; Score 40; DB 2; Length 96;
      Best Local Similarity 100.0%; Pred. No. 1.7;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 NMVPPFR 7
    |||||
Db  4 NMVPPFR 10

RESULT 23
O9CON6 ID Q9CON6 PRELIMINARY; PRT; 96 AA.
AC Q9CON6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium subglutinans.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
OC Gibberella fujikuroi complex.
OX NCBI_TaxID=42677;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MRC3478, and MRC7877;
RA Steenkamp E.T., Britz H., Coutinho T., Wingfield B., Marasas W.,
RA Wingfield M.;
RT "Molecular characterization of Fusarium subglutinans associated with
RT mango malformation.";
RL Mol. Plant Pathol. 1:187-193 (2000).
DR EMBL; AF236785; AAK08150.1; -.
DR EMBL; AF236786; AAK08151.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta tubulin.
DR InterPro; IPR008280; Tub_FtsZ_C.
DR Pfam; PF03953; Tubulin_C_1_.
DR PRINTS; PR01163; BETATUBULIN.
FT NON_TER      1
FT NON_TER      96
SQ SEQUENCE     96 AA; 11094 MW;  C735BB6745A4DBDD CRC64;

      Query Match      100.0%; Score 40; DB 2; Length 96;
      Best Local Similarity 100.0%; Pred. No. 1.7;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 NMVPPFR 7
    |||||
Db  7 NMVPPFR 13

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RESULT 24

Q9URJ0 PRELIMINARY; PRT; 96 AA.
 AC Q9URJ0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium sp. NRRL 25346.
 OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
 OC Hypocremycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OX NCBI_TaxID=122383;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL25346;
 RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
 RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
 species complex.";
 RL Mycologia 90:465-493(1998).
 DR EMBL: U61642; AAC26477.1; -;
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta_tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 FT NON TER 1 96
 FT NON TER 1 96
 SQ SEQUENCE 96 AA; 11096 MW; 23170D8308DD1D9E CRC64;

Query Match 100.0%; Score 40; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7

Db 8 NMVPPPR 14

RESULT 25

O74606 PRELIMINARY; PRT; 97 AA.
 AC O74606;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium beomiforme.
 OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
 OC Hypocremycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxID=44412;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL25174;
 RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
 RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
 species complex.";
 RL Mycologia 90:465-493(1998).
 DR EMBL: U61622; AAC26457.1; -;
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta_tubulin.

Qy 1 NMVPPPR 7

Db 7 NMVPPPR 13

RESULT 27
 Q6JIT3 PRELIMINARY; PRT; 97 AA.
 ID Q6JIT3
 AC Q6JIT3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)

DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 FT NON TER 1 97
 FT NON TER 1 97
 SQ SEQUENCE 97 AA; 10957 MW; 6125338E893FCD9F CRC64;

Query Match 100.0%; Score 40; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7

Db 8 NMVPPPR 14

RESULT 26

P78678 PRELIMINARY; PRT; 97 AA.
 AC P78678;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Gibberella circinata.
 OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
 OC Hypocremycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OX NCBI_TaxID=48490;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 22016;
 RX MEDLINE=97159566; PubMed=9007025; DOI=10.1006/mpev.1996.0376;
 RA O'Donnell K., Cigelnik E.;
 RT "Two divergent intragenomic rDNA ITS2 types within a monophyletic
 lineage of the fungus Fusarium are nonorthologous.";
 RL Mol. Phylogenet. Evol. 7:103-116(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 22016;
 RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
 RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
 species complex.";
 RL Mycologia 90:465-493(1998).
 DR EMBL: U34472; AAC26363.1; -;
 DR GO; GO:0045298; C:tubulin; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; P:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta_tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 FT NON TER 1 97
 FT NON TER 1 97
 SQ SEQUENCE 97 AA; 11225 MW; 8F6955BB6745A088 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPPR 7

Db 8 NMVPPPR 14

RESULT 27
 Q6JIT3 PRELIMINARY; PRT; 97 AA.
 ID Q6JIT3
 AC Q6JIT3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium sp. NRRL 29380.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxID=281088;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL29380;
 RX PubMed=15121083; DOI=10.1016/j.fgb.2004.03.003;
 RA O'Donnell K., Ward T.J., Geiser D.M., Corby Kistler H., Aoki T.;
 RT "Genealogical concordance between the mating type locus and seven
 RT other nuclear genes supports formal recognition of nine
 RT phylogenetically distinct species within the Fusarium graminearum
 RT Clade.";
 RL Fungal Genet. Biol. 41:600-623 (2004).
 DR EMBL; AY42951; AAT4592.1; -;
 DR GO; GO:0045298; F:GTP binding; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003924; F:GTPase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0046785; F:microtubule polymerization; IEA.
 DR GO; GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro; IPR002453; Beta tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PR01163; BETATUBULIN.
 DR NON_TER 1 1
 FT NON TER 97 97
 SQ SEQUENCE 97 AA; 11150 MW; A3EB917735BB6736 CRC64;

 Query Match 100.0%; Score 40; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 NMVPPFR 7
 DB |||||
 5 NMVPPFR 11

 RESULT 28
 Q9HDG4 PRELIMINARY; PRT; 97 AA.
 AC Q9HDG4; PRELIMINARY; PRT; 97 AA.
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Tubulin beta-2 chain (Fragment) (Beta-tubulin) (Fragment).
 GN Name: tub2;
 OS Gibberella zeae (Fusarium graminearum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=5518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL29169; NRRL28436; NRRL28723; NRRL29010; NRRL2903;
 RC NRRL28585; NRRL28718; NRRL25797; NRRL29148; NRRL29020; NRRL26916;
 RC NRRL29011; NRRL29105; NRRL26752; NRRL26754; NRRL26755; NRRL6101;
 RC NRRL13818; NRRL26156; NRRL28720; NRRL28721; NRRL5883; NRRL6394;
 RC NRRL13383; NRRL28063; NRRL28336; and NRRL28439;
 RX MEDLINE=20345085; PubMed=10869425; DOI=10.1073/pnas.130193297;
 RA O'Donnell K., Kistler H.C., Facke B.K., Casper H.H.;
 RT "Gene genealogies reveal global phylogeographic structure and
 RT reproductive isolation among lineages of Fusarium graminearum, the
 RT fungus causing wheat scab.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL29297; and NRRL29306;
 RX MEDLINE=22103635; PubMed=12080147; DOI=10.1073/pnas.142307199;
 RA Ward T.J., Bielawski J.P., Kistler H.C., Sullivan E., O'Donnell K.;
 RT "Ancestral polymorphism and adaptive evolution in the trichothecene

RT mycotoxin gene cluster of phytopathogenic Fusarium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9278-9283 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL29297; and NRRL29306;
 RA Ward T.J., Bielawski J.P., Kistler H.C., Sullivan E., O'Donnell K.;
 RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF212778; AAG43774.1; -;
 DR EMBL; AF212752; AAG43748.1; -;
 DR EMBL; AF212753; AAG43749.1; -;
 DR EMBL; AF212754; AAG43750.1; -;
 DR EMBL; AF212755; AAG43751.1; -;
 DR EMBL; AF212756; AAG43752.1; -;
 DR EMBL; AF212757; AAG43753.1; -;
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 DR EMBL; AF212945; AAG43941.1; -;
 DR EMBL; AF212946; AAG43942.1; -;
 DR EMBL; AF212947; AAG43943.1; -;
 DR EMBL; AF212948; AAG43944.1; -;
 DR EMBL; AF212949; AAG43945.1; -;
 DR EMBL; AF212950; AAG43946.1; -;
 DR EMBL; AF212951; AAG43947.1; -;
 DR EMBL; AF212952; AAG43948.1; -;
 DR EMBL; AF212953; AAG43949.1; -;
 DR EMBL; AF212954; AAG43950.1; -;
 DR EMBL; AF212955; AAG43951.1; -;
 DR EMBL; AF212956; AAG43952.1; -;
 DR EMBL; AF212957; AAG43953.1; -;
 DR EMBL; AF212958; AAG43954.1; -;
 DR EMBL; AF212959; AAG43955.1; -;
 DR EMBL; AF212960; AAG43956.1; -;
 DR EMBL; AF212961; AAG43957.1; -;
 DR EMBL; AF212962; AAG43958.1; -;
 DR EMBL; AF212963; AAG43959.1; -;
 DR EMBL; AF212964; AAG43960.1; -;
 DR EMBL; AF212965; AAG43961.1; -;
 DR EMBL; AF212966; AAG43962.1; -;
 DR EMBL; AF212967; AAG43963.1; -;
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 DR EMBL; AF212969; AAG43965.1; -;
 DR EMBL; AF212970; AAG43966.1; -;
 DR EMBL; AF212971; AAG43967.1; -;
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 DR EMBL; AF212973; AAG43969.1; -;
 DR EMBL; AF212974; AAG43970.1; -;
 DR EMBL; AF212975; AAG43971.1; -;
 DR EMBL; AF212976; AAG43972.1; -;
 DR EMBL; AF212977; AAG43973.1; -;
 DR EMBL; AF212978; AAG43974.1; -;
 DR EMBL; AF212979; AAG43975.1; -;
 DR EMBL; AF212980; AAG43976.1; -;
 DR EMBL; AF212981; AAG43977.1; -;
 DR EMBL; AF212982; AAG43978.1; -;
 DR EMBL; AF212983; AAG43979.1; -;
 DR EMBL; AF212984; AAG43980.1; -;
 DR EMBL; AF212985; AAG43981.1; -;
 DR EMBL; AF212986; AAG43982.1; -;
 DR EMBL; AF212987; AAG43983.1; -;
 DR EMBL; AF212988; AAG43984.1; -;
 DR EMBL; AF212989; AAG43985.1; -;
 DR EMBL; AF212990; AAG43986.1; -;
 DR EMBL; AF212991; AAG43987.1; -;
 DR EMBL; AF212992; AAG43988.1; -;
 DR EMBL; AF212993; AAG43989.1; -;
 DR EMBL; AF212994; AAG43990.1; -;
 DR EMBL; AF212995; AAG43991.1; -;
 DR EMBL; AF212996; AAG43992.1; -;
 DR EMBL; AF212997; AAG43993.1; -;
 DR EMBL; AF212998; AAG43994.1; -;
 DR EMBL; AF212999; AAG43995.1; -;
 DR EMBL; AF213000; AAG43996.1; -;
 DR EMBL; AF213001; AAG43997.1; -;
 DR EMBL; AF213002; AAG43998.1; -;
 DR EMBL; AF213003; AAG43999.1; -;
 DR EMBL; AF213004; AAG44000.1; -;
 DR EMBL; AF213005; AAG44001.1; -;
 DR EMBL; AF213006; AAG44002.1; -;
 DR EMBL; AF213007; AAG44003.1; -;
 DR EMBL; AF213008; AAG44004.1; -;
 DR EMBL; AF213009; AAG44005.1; -;
 DR EMBL; AF213010; AAG44006.1; -;
 DR EMBL; AF213011; AAG44007.1; -;
 DR EMBL; AF213012; AAG44008.1; -;
 DR EMBL; AF213013; AAG44009.1; -;
 DR EMBL; AF213014; AAG44010.1; -;
 DR EMBL; AF213015; AAG44011.1; -;
 DR EMBL; AF213016; AAG44012.1; -;
 DR EMBL; AF213017; AAG44013.1; -;
 DR EMBL; AF213018; AAG44014.1; -;
 DR EMBL; AF213019; AAG44015.1; -;
 DR EMBL; AF213020; AAG44016.1; -;
 DR EMBL; AF213021; AAG44017.1; -;
 DR EMBL; AF213022; AAG44018.1; -;
 DR EMBL; AF213023; AAG44019.1; -;
 DR EMBL; AF213024; AAG44020.1; -;
 DR EMBL; AF213025; AAG44021.1; -;
 DR EMBL; AF213026; AAG44022.1; -;
 DR EMBL; AF213027; AAG44023.1; -;
 DR EMBL; AF213028; AAG44024.1; -;
 DR EMBL; AF213029; AAG44025.1; -;
 DR EMBL; AF213030; AAG44026.1; -;
 DR EMBL; AF213031; AAG44027.1; -;
 DR EMBL; AF213032; AAG44028.1; -;
 DR EMBL; AF213033; AAG44029.1; -;
 DR EMBL; AF213034; AAG44030.1; -;
 DR EMBL; AF213035; AAG44031.1; -;
 DR EMBL; AF213036; AAG44032.1; -;
 DR EMBL; AF213037; AAG44033.1; -;
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 DR EMBL; AF213039; AAG44035.1; -;
 DR EMBL; AF213040; AAG44036.1; -;
 DR EMBL; AF213041; AAG44037.1; -;
 DR EMBL; AF213042; AAG44038.1; -;
 DR EMBL; AF213043; AAG44039.1; -;
 DR EMBL; AF213044; AAG44040.1; -;
 DR EMBL; AF213045; AAG44041.1; -;
 DR EMBL; AF213046; AAG44042.1; -;
 DR EMBL; AF213047; AAG44043.1; -;
 DR EMBL; AF213048; AAG44044.1; -;
 DR EMBL; AF213049; AAG44045.1; -;
 DR EMBL; AF213050; AAG44046.1; -;
 DR EMBL; AF213051; AAG44047.1; -;
 DR EMBL; AF213052; AAG44048.1; -;
 DR EMBL; AF213053; AAG44049.1; -;
 DR EMBL; AF213054; AAG44050.1; -;
 DR EMBL; AF213055; AAG44051.1; -;
 DR EMBL; AF213056; AAG44052.1; -;
 DR EMBL; AF213057; AAG44053.1; -;
 DR EMBL; AF213058; AAG44054.1; -;
 DR EMBL; AF213059; AAG44055.1; -;
 DR EMBL; AF213060; AAG44056.1; -;
 DR EMBL; AF213061; AAG44057.1; -;
 DR EMBL; AF213062; AAG44058.1; -;
 DR EMBL; AF213063; AAG44059.1; -;
 DR EMBL; AF213064; AAG44060.1; -;
 DR EMBL; AF213065; AAG44061.1; -;
 DR EMBL; AF213066; AAG44062.1; -;
 DR EMBL; AF213067; AAG44063.1; -;
 DR EMBL; AF213068; AAG44064.1; -;
 DR EMBL; AF213069; AAG44065.1; -;
 DR EMBL; AF213070; AAG44066.1; -;
 DR EMBL; AF213071; AAG44067.1; -;
 DR EMBL; AF213072; AAG44068.1; -;
 DR EMBL; AF213073; AAG44069.1; -;
 DR EMBL; AF213074; AAG44070.1; -;
 DR EMBL; AF213075; AAG44071.1; -;
 DR EMBL; AF213076; AAG44072.1; -;
 DR EMBL; AF213077; AAG44073.1; -;
 DR EMBL; AF213078; AAG44074.1; -;
 DR EMBL; AF213079; AAG44075.1; -;
 DR EMBL; AF213080; AAG44076.1; -;
 DR EMBL; AF213081; AAG44077.1; -;
 DR EMBL; AF213082; AAG44078.1; -;
 DR EMBL; AF213083; AAG44079.1; -;
 DR EMBL; AF213084; AAG44080.1; -;
 DR EMBL; AF213085; AAG44081.1; -;
 DR EMBL; AF213086; AAG44082.1; -;
 DR EMBL; AF213087; AAG44083.1; -;
 DR EMBL; AF213088; AAG44084.1; -;
 DR EMBL; AF213089; AAG44085.1; -;
 DR EMBL; AF213090; AAG44086.1; -;
 DR EMBL; AF213091; AAG44087.1; -;
 DR EMBL; AF213092; AAG44088.1; -;
 DR EMBL; AF213093; AAG44089.1; -;
 DR EMBL; AF213094; AAG44090.1; -;
 DR EMBL; AF213095; AAG44091.1; -;
 DR EMBL; AF213096; AAG44092.1; -;
 DR EMBL; AF213097; AAG44093.1; -;
 DR EMBL; AF213098; AAG44094.1; -;
 DR EMBL; AF213099; AAG44095.1; -;
 DR EMBL; AF213100; AAG44096.1; -;
 DR EMBL; AF213101; AAG44097.1; -;
 DR EMBL; AF213102; AAG44098.1; -;
 DR EMBL; AF213103; AAG44099.1; -;
 DR EMBL; AF213104; AAG44100.1; -;
 DR EMBL; AF213105; AAG44101.1; -;
 DR EMBL; AF213106; AAG44102.1; -;
 DR EMBL; AF213107; AAG44103.1; -;
 DR EMBL; AF2

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OX NCBI_TaxID=5516;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25475, and NRRL3288;
RX MEDLINE=20345085; PubMed=10869425; DOI=10.1073/pnas.130193297;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR EMBL; AF212780; AAG43776.1; -
DR EMBL; AF212779; AAG43775.1; -
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
DR NON_TER 97
FT NON_TER 97
SQ SEQUENCE 97 AA; 11150 MW; A3EB917735BB6736 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 5 NMVPPFR 11

RESULT 30
Q9HDG6 ID Q9HDG6 PRELIMINARY; PRT; 97 AA.
AC Q9HDG6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tubulin beta-2 chain (Fragment) (Fragment).
GN Name=tub2;
OS Fusarium cerealis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=56641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL3393, NRRL13721, NRRL25491, and NRRL25805;
RX MEDLINE=20345085; PubMed=10869425; DOI=10.1073/pnas.130193297;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR EMBL; AF212784; AAG43780.1; -
DR EMBL; AF212781; AAG43777.1; -
DR EMBL; AF212782; AAG43778.1; -
DR EMBL; AF212783; AAG43779.1; -
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
DR NON_TER 97
FT NON_TER 97

Query Match 100.0%; Score 40; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 5 NMVPPFR 11

RESULT 31
Q9HDG7 ID Q9HDG7 PRELIMINARY; PRT; 97 AA.
AC Q9HDG7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tubulin beta-2 chain (Fragment) (Fragment).
GN Name=tub2;
OS Fusarium pseudograminearum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=101028;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL28338, NRRL28062, NRRL28065, and NRRL28334;
RX MEDLINE=20345085; PubMed=10869425; DOI=10.1073/pnas.130193297;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR EMBL; AF212788; AAG43784.1; -
DR EMBL; AF212785; AAG43781.1; -
DR EMBL; AF212786; AAG43782.1; -
DR EMBL; AF212787; AAG43783.1; -
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
DR NON_TER 97
FT NON_TER 97
SQ SEQUENCE 97 AA; 11150 MW; A3EB917735BB6736 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
Db 5 NMVPPFR 11

RESULT 32
Q9P4G7 ID Q9P4G7 PRELIMINARY; PRT; 97 AA.
AC Q9P4G7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium sp. NRRL 25623.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=100623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL13393, NRRL13721, NRRL25491, and NRRL25805;
RX MEDLINE=20345085; PubMed=10869425; DOI=10.1073/pnas.130193297;
RA O'Donnell K., Kistler H.C., Tacke B.K., Casper H.H.;
RT "Gene genealogies reveal global phylogeographic structure and
RT reproductive isolation among lineages of Fusarium graminearum, the
RT fungus causing wheat scab.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7905-7910(2000).
DR EMBL; AF212784; AAG43780.1; -
DR EMBL; AF212781; AAG43777.1; -
DR EMBL; AF212782; AAG43778.1; -
DR EMBL; AF212783; AAG43779.1; -
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01163; BETATUBULIN.
DR NON_TER 1
DR NON_TER 97
FT NON_TER 97

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DR GO: GO:0003924; F:GTPase activity; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0046785; P:microtubule polymerization; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR002453; Beta tubulin.
 DR InterPro: IPR008280; Tub_FtsZ_C.
 DR Pfam: PF03953; Tubulin_C; 1.
 DR PRINTS: PRO1163; BETATUBULIN.
 FT NON_TER 1
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 11306 MW; 665B33170D8308DD CRC64;

Query Match 100.0%; Score 40; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 |||||
 Db 8 NMVPPFR 14

RESULT 36

O74607 PRELIMINARY; PRT; 98 AA.
 AC O74607;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Fusarium brevicatenuatum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OX NCBI_TaxID=48488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL25446;
 RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
 RT "Molecular systematics and phylogeography of the Gibberella fujikuroi species complex.";
 RL Mycologia 90:465-493 (1998).
 DR EMBL: U61623; AAC26458.1; -.
 DR GO: GO:0045298; C:tubulin; IEA.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0003924; F:GTPase activity; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0046785; P:microtubule polymerization; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR002453; Beta tubulin.
 DR Pfam: PF03953; Tubulin_C; 1.
 DR PRINTS: PRO1163; BETATUBULIN.
 FT NON_TER 1
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 11333 MW; 665B330D248308DD CRC64;

Query Match 100.0%; Score 40; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 |||||
 Db 8 NMVPPFR 14

RESULT 37

O74608 PRELIMINARY; PRT; 98 AA.
 AC O74608;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).

OS Fusarium bulbicola.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OX NCBI_TaxID=79018;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL13618;
 RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
 RT "Molecular systematics and phylogeography of the Gibberella fujikuroi species complex.";
 RL Mycologia 90:465-493 (1998).
 DR EMBL: U61624; AAC26459.1; -.
 DR GO: GO:0045298; C:tubulin; IEA.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0003924; F:GTPase activity; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0046785; P:microtubule polymerization; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR002453; Beta tubulin.
 DR InterPro: IPR008280; Tub_FtsZ_C.
 DR Pfam: PF03953; Tubulin_C; 1.
 DR PRINTS: PRO1163; BETATUBULIN.
 FT NON_TER 1
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 11306 MW; 665B33170D8308DD CRC64;

Query Match 100.0%; Score 40; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 |||||
 Db 8 NMVPPFR 14

RESULT 38

O74609 PRELIMINARY; PRT; 98 AA.
 AC O74609;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-tubulin (Fragment).
 OS Gibberella circinata.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OX NCBI_TaxID=48490;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL25331;
 RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
 RT "Molecular systematics and phylogeography of the Gibberella fujikuroi species complex.";
 RL Mycologia 90:465-493 (1998).
 DR EMBL: U61625; AAC26460.1; -.
 DR GO: GO:0045298; C:tubulin; IEA.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0003924; F:GTPase activity; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0046785; P:microtubule polymerization; IEA.
 DR GO: GO:0007018; P:microtubule-based movement; IEA.
 DR InterPro: IPR002453; Beta tubulin.
 DR InterPro: IPR008280; Tub_FtsZ_C.
 DR Pfam: PF03953; Tubulin_C; 1.
 DR PRINTS: PRO1163; BETATUBULIN.
 FT NON_TER 1
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 11306 MW; 665B33170D8308DD CRC64;

Query Match 100.0%; Score 40; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPPFR 7
 |||||
 Db 8 NMVPPFR 14

Query Match 100.0%; Score 40; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 8 NMVPFPR 14

RESULT 39

O74610 PRELIMINARY; PRT; 98 AA.
ID O74610
AC O74610;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium concentricum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
OC Gibberella fujikuroi complex.
OX NCBI_TaxID=48491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25181;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex."; 493 (1998).
RL Mycologia 90:465-493 (1998).
RE ENBL; U61626; AAC26461.1; -.
DR GO; GO:0045298; C:tubulin; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR02453; Beta tubulin.
DR InterPro; IPR008280; Tub_FtsZ_C.
DR Pfam; PF03953; Tubulin_C_1.
DR PRINTS; PR01163; BETATUBULIN.
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 11306 MW; 665833170D8308DD CRC64;

Query Match 100.0%; Score 40; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 8 NMVPFPR 14

RESULT 40

O74612 PRELIMINARY; PRT; 98 AA.
ID O74612
AC O74612;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-tubulin (Fragment).
OS Fusarium denticulatum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
OC Gibberella fujikuroi complex.
OX NCBI_TaxID=48507;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL25302;
RA O'Donnell K., Cigelnik E., Nirenberg H.I.;
RT "Molecular systematics and phylogeography of the Gibberella fujikuroi
species complex."; 493 (1998).
RL Mycologia 90:465-493 (1998).
RE ENBL; U61628; AAC26463.1; -.
DR GO; GO:0045298; C:tubulin; IEA.

DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046785; P:microtubule polymerization; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR02453; Beta tubulin.
DR InterPro; IPR008280; Tub_FtsZ_C.
DR Pfam; PF03953; Tubulin_C_1.
DR PRINTS; PR01163; BETATUBULIN.
FT NON_TER 1
FT NON_TER 98
SQ SEQUENCE 98 AA; 11333 MW; 665B330D248308DD CRC64;
Query Match 100.0%; Score 40; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMVPFPR 7
Db 8 NMVPFPR 14

Search completed: July 20, 2005, 17:31:31
Job time : 60.6296 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 17:16:22 ; Search time 97.037 Seconds
(without alignments)
79.714 Million cell updates/sec

Title: US-10-766-480A-2

Perfect score: 110

Sequence: 1 ASAFQIGSTHWYDVGNS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	95.5	652	4	ABG27471 Novel hum
2	105	95.5	1250	8	ABM83979 Human dia
3	77	70.0	747	4	ABG11969 Novel hum
4	77	70.0	809	5	AAE15983 Human CNG
5	77	70.0	809	5	AAE15984 Human CNG
6	77	70.0	809	5	AAE15985 Human CNG
7	77	70.0	809	5	AAE15986 Human CNG
8	77	70.0	809	5	AAE15982 Human CNG
9	53	48.2	123	4	ABH12369 Human bon
10	53	48.2	1037	4	ABH66545 Drosophila
11	50	45.5	250	7	ADC00523 Enterohae
12	50	45.5	250	7	ADB99971 Enterohae
13	49	44.5	54	3	AAE154437 Peptide w
14	49	44.5	497	7	ABO76390 Pseudomon
15	49	44.5	934	4	ABH60394 Drosophila
16	48	43.6	246	7	ADC00617 Enterohae
17	48	43.6	303	7	ABO80278 Pseudomon
18	48	43.6	621	8	ADZ28014 Bacterial
19	47	42.7	246	7	AAE60874 Modified
20	47	42.7	246	2	AAE90301 Modified
21	47	42.7	246	2	AAE93201 Gpv prote
22	47	42.7	246	2	AAE93202 C-termina
23	47	42.7	246	2	AAW24580 Modified
24	47	42.7	246	2	AAW22851 Fusion pr
25	47	42.7	246	6	ABG73548 Phage maj

26	47	42.7	292	2	AAW22850 Fusion pr
27	47	42.7	292	6	ABG73549 Lambda-fo
28	47	42.7	946	6	ABR52676 Protein s
29	47	42.7	946	6	ABP57428 Saccharom
30	47	42.7	946	7	ADK61804 Disease t
31	46.5	42.3	170	6	ABU61683 Program d
32	46.5	42.3	170	7	ADB66814 Potassiu
33	46	41.8	35	4	AAE10074 Human ion
34	46	41.8	35	6	ABU97335 Amino aci
35	46	41.8	35	7	ADG29253 Novel hum
36	46	41.8	126	4	ABG07100 Novel hum
37	46	41.8	247	7	ADC00916 Enterohae
38	46	41.8	322	2	AAE52025 Bacillus
39	46	41.8	447	3	ABH36460 Lemon acy
40	45.5	41.4	128	4	AAAM00034 Endoxylag
41	45.5	41.4	200	4	AAAM00096 Endoxylag
42	45.5	41.4	327	6	ABU45124 Protein e
43	45.5	41.4	328	6	ABU47080 Protein e
44	45.5	41.4	328	6	ABU47590 Protein e
45	45.5	41.4	648	8	ADS28159 Bacterial

ALIGNMENTS

RESULT 1
ABG27471
ID ABG27471 standard; protein; 652 AA.
XX AC ABG27471;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #27462.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-ESDB; RAS91658.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PS Claim 20; SEQ ID NO 57830; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridization probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
XX CC in and recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 652 AA;

Query Match 95.5%; Score 105; DB 4; Length 652;
Best Local Similarity 90.0%; Pred. No. 6.8e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDVGNS 20
|||:|||||
Db 213 ASAYQGLGSTHWYDVGNS 232

RESULT 2

ABM83979
ID ABM83979 standard; protein; 1250 AA.

XX AC
XX ABM83979;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4228.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

XX PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;

XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

XX PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX PI Patuary S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

XX DR N-PSDB; ACN42631.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX PT in diagnosing a condition, disease or disorder associated with human

XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides

CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 1250 AA;

Query Match 95.5%; Score 105; DB 8; Length 1250;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDVGNS 20
|||:|||||
Db 811 ASAYQGLGSTHWYDVGNS 830

RESULT 3

ABG11969

ID ABG11969 standard; protein; 747 AA.

XX AC
XX ABG11969;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #11960.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS76156.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity.

XX PS Claim 20; SEQ ID NO 42328; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX CC sequences. (I) is useful as hybridisation probes, polymerase chain

XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

XX CC and in recombinant production of (II). The polynucleotides are also used

XX CC in diagnostics as expressed sequence tags for identifying expressed

XX CC genes. (I) is useful in gene therapy techniques to restore normal

XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AEG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 747 AA;

Query Match 70.0%; Score 77; DB 4; Length 747;
 Best Local Similarity 68.4%; Pred. No. 0.011;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGISTHWYDGVGN 19
 ||:||||:||||||
 Db 728 ASNYEGIGTTRWYDGEEN 746

RESULT 4
 AAE15983
 ID AAE15983 standard; protein; 809 AA.
 XX
 AC AAE15983;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human CNG3B protein variant #1 (R142K).
 XX
 KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
 KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
 KW male infertility; genetic defect; reporter-ligand interaction; CNG;
 KW viral infection; cancer; mutant; mutein; variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 142 /note= "Wild type Arg substituted with Lys"
 XX
 FN WO20018090-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 15-MAY-2001; 2001WO-US015814.
 XX
 PR 15-MAY-2000; 2000US-0204445P.
 PR 14-MAY-2001; 2001US-00855828.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Creech CD, Jegla TJ;
 XX
 DR WPI; 2002-089847/12.
 XX
 PT New polypeptide, useful for screening for modulators of cyclic nucleotide
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
 PT cation channel 3 beta subunit.
 XX
 PS Disclosure; Page; 83pp; English.
 XX
 CC The invention relates to human cyclic nucleotide-gated cation channel 3
 CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 CC subunits that are expressed in retina. CNG3B polypeptides are useful for
 CC screening modulators of CNGs which are useful as contraceptives and for
 CC treating various disorders involving cation channels, e.g. vision
 CC disorders and male infertility. Polynucleotides of the invention are
 CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.

CC Sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is human CNG3B protein variant
 CC (R142K). Note: This sequence is not shown in the specification, but is
 CC derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig
 CC 4 of the specification (AAE15982)
 XX
 SQ Sequence 809 AA;

Query Match 70.0%; Score 77; DB 5; Length 809;
 Best Local Similarity 68.4%; Pred. No. 0.012;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGISTHWYDGVGN 19
 ||:||||:||||||
 Db 374 ASNYEGIGTTRWYDGEEN 392

RESULT 5
 AAE15984
 ID AAE15984 standard; protein; 809 AA.
 XX
 AC AAE15984;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human CNG3B protein variant #2 (D154N).
 XX
 KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
 KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
 KW male infertility; genetic defect; reporter-ligand interaction; CNG;
 KW viral infection; cancer; mutant; mutein; variant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 154 /note= "Wild type Asp substituted with Asn"
 XX
 FN WO20018090-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 15-MAY-2001; 2001WO-US015814.
 XX
 PR 15-MAY-2000; 2000US-0204445P.
 PR 14-MAY-2001; 2001US-00855828.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Creech CD, Jegla TJ;
 XX
 DR WPI; 2002-089847/12.
 XX
 PT New polypeptide, useful for screening for modulators of cyclic nucleotide
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
 PT cation channel 3 beta subunit.
 XX
 PS Disclosure; Page; 83pp; English.
 XX
 CC The invention relates to human cyclic nucleotide-gated cation channel 3
 CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 CC subunits that are expressed in retina. CNG3B polypeptides are useful for
 CC screening modulators of CNGs which are useful as contraceptives and for
 CC treating various disorders involving cation channels, e.g. vision
 CC disorders and male infertility. Polynucleotides of the invention are
 CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.

CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.
 CC Sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is human CNG3B protein variant
 CC (D154N). Note: This sequence is not shown in the specification, but is
 CC derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig
 CC 4 of the specification (AAE15982)
 XX
 SQ Sequence 809 AA;

Query Match 70.0%; Score 77; DB 5; Length 809;
 Best Local Similarity 68.4%; Pred. No. 0.012;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASAFQIGIGSTHWYDGVGN 19
 || :|||:|||||
 Db 374 ASNYEGIGTRWYDGEEN 392

RESULT-6
 AAE15985
 ID AAE15985 standard; protein; 809 AA.
 XX
 AC AAE15985;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human CNG3B protein variant #3 (L675V).

XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
 KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
 KW male infertility; genetic defect; reporter-ligand interaction; CNG;
 KW viral infection; cancer; mutant; mutein; variant.

XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 675
 FT /note= "Wild type Leu substituted with Val"
 XX
 XX WO20018090-A2.

XX
 XX 22-NOV-2001.
 XX
 XX 15-MAY-2001; 2001WO-US015814.
 XX
 XX 15-MAY-2000; 2000US-0204445P.
 XX 14-MAY-2001; 2001US-00855828.
 XX (ICAG-) ICAGEN INC.
 XX
 XX Creech CD, Jegla TJ;
 XX WPI; 2002-089847/12.
 XX
 XX New polypeptide, useful for screening for modulators of cyclic nucleotide
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
 PT cation channel 3 beta subunit.
 XX
 XX Disclosure; Page; 83pp; English.

XX The invention relates to human cyclic nucleotide-gated cation channel 3
 CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 CC subunits that are expressed in retina. CNG3B polypeptides are useful for
 CC screening modulators of CNGs which are useful as contraceptives and for

CC treating various disorders involving cation channels, e.g. vision
 CC disorders and male infertility. Polynucleotides of the invention are
 CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.
 CC Sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is human CNG3B protein variant
 CC (L675V). Note: This sequence is not shown in the specification, but is
 CC derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig
 CC 4 of the specification (AAE15982)
 XX
 SQ Sequence 809 AA;

Query Match 70.0%; Score 77; DB 5; Length 809;
 Best Local Similarity 68.4%; Pred. No. 0.012;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASAFQIGIGSTHWYDGVGN 19
 || :|||:|||||
 Db 374 ASNYEGIGTRWYDGEEN 392

RESULT 7
 AAE15986
 ID AAE15986 standard; protein; 809 AA.
 XX
 AC AAE15986;
 XX

XX 26-MAR-2002 (first entry)
 XX
 DE Human CNG3B protein variant #4 (G682S).
 XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
 KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
 KW male infertility; genetic defect; reporter-ligand interaction; CNG;
 KW viral infection; cancer; mutant; mutein; variant.

XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 682
 FT /note= "Wild type Gly substituted with Ser"
 XX
 XX WO20018090-A2.

XX
 XX 22-NOV-2001.
 XX
 XX 15-MAY-2001; 2001WO-US015814.
 XX
 XX 15-MAY-2000; 2000US-0204445P.
 XX 14-MAY-2001; 2001US-00855828.
 XX (ICAG-) ICAGEN INC.
 XX
 XX Creech CD, Jegla TJ;
 XX WPI; 2002-089847/12.
 XX
 XX New polypeptide, useful for screening for modulators of cyclic nucleotide
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
 PT cation channel 3 beta subunit.
 XX
 XX Disclosure; Page; 83pp; English.

XX The invention relates to human cyclic nucleotide-gated cation channel 3
 CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 CC subunits that are expressed in retina. CNG3B polypeptides are useful for

CC subunits that are expressed in retina. CNG3B polypeptides are useful for
 CC screening modulators of CNGs which are useful as contraceptives and for
 CC treating various disorders involving cation channels, e.g. vision
 CC disorders and male infertility. Polynucleotides of the invention are
 CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.
 CC sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is human CNG3B protein (SEQ ID NO:1) shown in Fig
 CC 4 of the specification (AAE15982)

XX Sequence 809 AA;

Query Match 70.0%; Score 77; DB 5; Length 809;
 Best Local Similarity 68.4%; Pred. No. 0.012;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVGN 19
 || :|||: ||||| ||
 Db 374 ASNYEGIGTRWYDGEEN 392

RESULT 8
 AAE15982
 ID AAE15982 standard; protein; 809 AA.
 XX
 AC AAE15982;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human cyclic nucleotide-gated cation channel 3 beta subunit protein.

XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
 KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
 KW male infertility; genetic defect; reporter-ligand interaction; CNG;
 KW viral infection; cancer.
 XX
 OS Homo sapiens.

EH Key Location/Qualifiers
 FT Region 210..661
 FT /note= "Conserved region; this region also function as an
 FT epitope and is referred in claim 1"

XX WO200188090-A2.

PD 22-NOV-2001.

XX 15-MAY-2001; 2001WO-US015814.

PR 15-MAY-2000; 2000US-0204445P.

PR 14-MAY-2001; 2001US-00855828.

XX (ICAG-) ICAGEN INC.

XX Creech CD, Jegla TJ;

DR WPI; 2002-089847/12.

DR N-PSDB; AAD25729.

XX New polypeptide, useful for screening for modulators of cyclic nucleotide
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
 PT cation channel 3 beta subunit.

XX Claim 12; Fig 4; 83pp; English.

XX The invention relates to human cyclic nucleotide-gated cation channel 3

CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 CC subunits that are expressed in retina. CNG3B polypeptides are useful for
 CC screening modulators of CNGs which are useful as contraceptives and for
 CC treating various disorders involving cation channels, e.g. vision
 CC disorders and male infertility. Polynucleotides of the invention are
 CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.
 CC Sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is human CNG3B protein

XX Sequence 809 AA;

Query Match 70.0%; Score 77; DB 5; Length 809;
 Best Local Similarity 68.4%; Pred. No. 0.012;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVGN 19
 || :|||: ||||| ||
 Db 374 ASNYEGIGTRWYDGEEN 392

RESULT 9
 ABB12369
 ID ABB12369 standard; protein; 123 AA.

XX ABB12369;

DT 15-JAN-2002 (first entry)

XX Human bone marrow expressed protein SEQ ID NO: 124.

XX Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;
 KW antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
 KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
 KW antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;
 KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
 KW nervous system disorder; autoimmune disorder; inflammation; allergy.

XX Homo sapiens.

XX WO200174836-A1.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US010472.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PR 30-NOV-2000; 2000US-0250583P.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;

XX WPI; 2001-626375/72.

DR N-PSDB; ABA09614.

XX New bone marrow-expressed nucleic acids and polypeptides, useful for
 PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
 PT and increasing hematopoiesis, stem cell survival and bone growth and
 PT remodeling.

XX Claim 10; Page 229; 380pp; English.

XX The present invention relates to bone marrow expressed polynucleotides
 CC and proteins. These sequences can be used in the treatment of

XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 25136; 455pp; English.
XX
XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-*P. aeruginosa* drugs, as templates for recombinant
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
CC infection, and in detection of *P. aeruginosa* sequences or other sequences
CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-
CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 497 AA;

Query Match 44.5%; Score 49; DB 7; Length 497;
Best Local Similarity 69.2%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 GSTHWVYDGVGNS 20
Db 113 GMTYGVYDAGNS 125

RESULT 15
AB060394
ID ABB60394 standard; protein; 934 AA.
XX
XX ABB60394;
XX
XX 26-MAR-2002 (first entry)
XX
XX *Drosophila melanogaster* polypeptide SEQ ID NO 7974.
XX
XX *Drosophila*; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX *Drosophila melanogaster*.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL04497.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
PT interactions.
XX
XX Disclosure; SEQ ID NO 7974; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 934 AA;

Query Match 44.5%; Score 49; DB 4; Length 934;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVG 18
Db 776 AGAFAAVVSTHWADGGAG 793

RESULT 16
ADC00617
ID ADC00617 standard; protein; 246 AA.
XX
XX ADC00617;

XX
XX 04-DEC-2003 (first entry)
XX
XX Enterohaemorrhagic *E. coli* O157:H7-specific protein SEQ ID NO: 662.
XX
XX enterohaemorrhagic; anti-bacterial.
XX
XX *Escherichia coli*; O157:H7.
XX
XX JP2002355074-A.
XX
XX 10-DEC-2002.

XX 24-JAN-2002; 2002JP-00015959.

XX 24-JAN-2001; 2001JP-00112010.

XX (UYTS-) UNIV TSUKUBA.

XX WPI; 2003-451640/43.

XX Enterohaemorrhagic *Escherichia coli* O157:H7-specific nucleic acid molecule
XX and a polypeptide and its use, a polypeptide, a vector and a host cell.

XX Claim 3; SEQ ID NO 662; 2067pp; Japanese.

XX The invention relates to a novel enterohaemorrhagic *Escherichia coli*
CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC has anti-bacterial activity. The polypeptide can be used in detection
CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC genome of Enterohaemorrhagic *E. coli* O157:H7 was determined. The present
CC invention represents an *E. coli* O157:H7-specific polypeptide of the
CC invention.

XX Sequence 246 AA;

Query Match 43.6%; Score 48; DB 7; Length 246;
Best Local Similarity 53.3%; Pred. No. 66;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19

Db 11 KGAGTTLWVINGND 25

RESULT 17
AB080278

ID AB080278 standard; protein; 303 AA.
AC AB080278;
DT 29-JUL-2004 (first entry)
XX Pseudomonas aeruginosa polypeptide #12453.
DE
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
KW Pseudomonas aeruginosa.
OS
XX US551795-B1.
FN
XX 22-APR-2003.
PD
XX 18-FEB-1999; 99US-00252991.
PP
XX 18-FEB-1998; 98US-0074788P.
PR
XX 27-JUL-1998; 98US-0094190P.
PR
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
FI
XX WPI; 2003-615309/58.
DR
XX N-PSDB; ABD13849.
DR
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 29024; 455pp; English.
PS
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences AB067826-
CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX SQ Sequence 303 AA;
Query Match 43.6%; Score 48; DB 7; Length 303;
Best Local Similarity 50.0%; Pred. No. 83;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ASAFQGGSTHWVDGVG 18
Db 198 AAAPFGLGQRHLAGGVG 215
RESULT 18
ADS28014
ID ADS28014 standard; protein; 621 AA.
XX
AC ADS28014;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #17047.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
FN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
PP
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
FI
XX WPI; 2004-Q61375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 17047; 122pp; English.
PS
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 621 AA;
Query Match 43.6%; Score 48; DB 8; Length 621;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ASAFQGGSTHWVDGVG 18
Db 388 ATETQGITVTHWITERVG 405
RESULT 19
AAR60874
ID AAR60874 standard; protein; 246 AA.
XX

AC AAR60874;
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 14-JUL-1995 (first entry)
 XX
 DE Modified GpV protein of lambdaoid bacteriophage.
 XX
 KW Bacteriophage; GpV; assay; detection; modification; lambdaoid.
 XX
 OS Bacteriophage lambda.
 XX
 PN WO9424959-A1.
 XX
 PD 10-NOV-1994.
 XX
 XX 28-APR-1994; 94WO-US004611.
 PF
 XX 27-APR-1993; 93US-00053866.
 PR
 XX (SYMB-) SYMBIOTECH INC.
 PA
 XX Ray BL, Lin ECC, Crea R;
 PI
 XX WPI; 1994-357835/44.
 DR
 DR N-PSDB; AAQ73779.
 DR
 XX Infective lambdaoid bacteriophage - useful for detecting compounds of
 PT interest.
 PT
 XX
 PS Claim 19; Page 29; 56pp; English.
 PS
 XX A lambdaoid bacteriophage having a chemically modified GpV protein can be
 CC used as an assay system for molecules of interest. The bacteriophage,
 CC having a target molecule chemically linked to one of its components, the
 CC GpV protein, can be successfully assembled in vitro so that the target
 CC molecule is displayed on the outer surface of the phage. The chemically
 CC modified phage retains the ability to infect E.coli. The bacteriophage is
 CC processed to be non-infective. The presence of a molecule of interest
 CC renders the phage infective again and thus, this system can be used in a
 CC detection method. The modified GpV protein comprises a chemically
 CC reactive amino acid residue selected from His, Cys (pref.), Trp and Tyr
 CC and this residue is located at the C-terminal end. (Updated on 25-MAR-
 CC 2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
 CC
 XX Sequence 246 AA;
 SQ
 Query Match 42.7%; Score 47; DB 2; Length 246;
 Best Local Similarity 53.3%; Pred. No. 93;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QGIGSTHWYDGVGN 19
 :|:|:|:|:|:|:
 Db 11 KGAGTTLWVYKSGD 25
 RESULT 20
 AAR90301
 ID AAR90301 standard; protein; 246 AA.
 AC
 XX
 XX AAR90301;
 XX
 DT 22-JUL-1996 (first entry)
 XX
 DE Modified gpV protein.
 XX
 KW gpV; modified; lambdaoid bacteriophage; outer surface; expression;
 KW foreign protein.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 246
 FT

FT
 XX
 PN WO9534683-A1.
 XX
 PD 21-DEC-1995.
 XX
 XX 10-JUN-1994; 94WO-US006543.
 PF
 XX 10-JUN-1994; 94WO-US006543.
 PR
 XX (SYMB-) SYMBIOTECH INC.
 PA
 XX Ray BL, Lin ECC, Crea R;
 PI
 XX WPI; 1996-049709/05.
 DR
 DR N-PSDB; AAT11701.
 DR
 XX Modified infectious lambdaoid phage - contg. gpV/target molecule fusion
 PT peptide, useful for detecting bioactive cpds. and cells that express
 PT them.
 PT
 XX Example 1; Page 39-40; 67pp; English.
 PS
 XX The present sequence is that of a modified V protein, where the carboxy
 CC terminal Ser246 is replaced with a Cys. Lambdaoid bacteriophage can express
 CC this modified gpV having a target mol. peptide bonded to the carboxy
 CC terminus so as to expose the target molecule on the outer surface of its
 CC tail. Such infectious bacteriophage are useful to detect biological
 CC active cpds. and to select cells that express them. A partic. application
 CC is screening enzyme libraries for clones that cleave altered substrates
 CC
 XX Sequence 246 AA;
 SQ
 Query Match 42.7%; Score 47; DB 2; Length 246;
 Best Local Similarity 53.3%; Pred. No. 93;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QGIGSTHWYDGVGN 19
 :|:|:|:|:|:|:
 Db 11 KGAGTTLWVYKSGD 25
 RESULT 21
 AAR93201
 ID AAR93201 standard; protein; 246 AA.
 AC
 XX
 XX AAR93201;
 XX
 DT 01-JUN-1996 (first entry)
 XX
 DE GpV protein.
 XX
 KW GpV protein; major tail protein; fusion protein; conjugate; mutant;
 KW strain improvement; metabolic engineering; enzyme; substrate;
 KW immunoglobulin; receptor; ligand; matrix; starter cell; auxotroph;
 KW phage resistance; cross-feeding; feeder cell; Escherichia coli;
 KW screening.
 XX
 OS Bacteriophage lambda.
 XX
 PN WO9606164-A1.
 XX
 PD 29-FEB-1996.
 XX
 XX 10-AUG-1995; 95WO-US010224.
 PF
 XX 23-AUG-1994; 94US-00294386.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Ray BL, Lin ECC, Crea R;
 PI
 XX WPI; 1996-151367/15.
 DR

DR N-PSDB; AAT16734.

XX Isolating mutant cells that produce required cpd. - by culture with

PT auxotrophic feeder cells and reversibly non-infecting phage, growth only

PT being possible if specified cpd. is produced.

XX

PS Disclosure; Page 69; 100pp; English.

XX

CC The sequence represents a phage lambda gpv major tail protein. The

CC protein may be truncated and a reactive cysteine residue inserted (as in

CC AAR93202) for production of a fusion protein or crosslinked conjugate.

CC The modified protein forms part of a system for isolation of mutant cells

CC producing a desired compound (e.g. an enzyme, substrate, immunoglobulin,

CC receptor, ligand or matrix). A starter cell, which is an auxotroph for a

CC 1st metabolite, is phage lambda resistant and secretes a 2nd metabolite,

CC is cocultured with a feeder cell (preferably Escherichia coli) which

CC requires the 2nd metabolite and a nutrient, is phage lambda susceptible

CC and secretes the 1st metabolite, in the presence of a lambdaoid phage

CC which has reduced or no capacity for lytic infection, carries a gene

CC encoding the feeder cell nutrient, and carries a modified gpv protein, to

CC which a target protein is linked and bound to a ligand which renders the

CC phage reversibly non-infective. The phage becomes infective if a starter

CC cell secretes the desired product. Colonies are isolated, and starter

CC cells producing the desired product are selected. The system may be used

CC in metabolic engineering and screening for new activities, and is

CC applicable to a wide variety of starter cell types

XX

SQ Sequence 246 AA;

Query Match 42.7%; Score 47; DB 2; Length 246;

Best Local Similarity 53.3%; Pred. No. 93;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 5 OGIGSTHWYDGVGN 19

Db 11 KGAGTTLWYKSGD 25

RESULT 22

AAR93202

ID AAR93202 standard; protein; 246 AA.

XX

AC AAR93202;

XX

DT 01-JUN-1996 (first entry)

XX

DE C-terminally modified gpv protein.

XX

KW Gpv protein; major tail protein; C-terminus; modification;

KW fusion protein; conjugate; mutant; strain improvement;

KW metabolic engineering; enzyme; substrate; immunoglobulin; receptor;

KW ligand; matrix; starter cell; auxotroph; phage resistance; cross-feeding;

KW feeder cell; Escherichia coli; screening.

XX

OS Bacteriophage lambda.

XX

PN WO9606164-A1.

XX

PD 29-FEB-1996.

XX

PF 10-AUG-1995; 95WO-US010224.

XX

PR 23-AUG-1994; 94US-00294386.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Ray BL, Lin ECC, Crea R;

XX

XX WPI; 1996-151367/15.

DR N-PSDB; AAT16734.

XX

PT Isolating mutant cells that produce required cpd. - by culture with

PT auxotrophic feeder cells and reversibly non-infecting phage, growth only

PT being possible if specified cpd. is produced.

XX

PS Disclosure; Page 71; 100pp; English.

XX

CC The sequence represents a phage lambda gpv major tail protein, with a

CC reactive cysteine residue inserted at the C-terminus for production of a

CC fusion protein or crosslinked conjugate. The modified protein forms part

CC of a system for isolation of mutant cells producing a desired compound

CC (e.g. an enzyme, substrate, immunoglobulin, receptor, ligand or matrix).

CC A starter cell, which is an auxotroph for a 1st metabolite, is phage

CC lambda resistant and secretes a 2nd metabolite, is cocultured with a

CC feeder cell (preferably Escherichia coli) which requires the 2nd

CC metabolite and a nutrient, is phage lambda susceptible and secretes the

CC 1st metabolite, in the presence of a lambdaoid phage which has reduced or

CC no capacity for lytic infection, carries a gene encoding the feeder cell

CC nutrient, and carries a modified gpv protein, to which a target protein

CC is linked and bound to a ligand which renders the phage reversibly non-

CC infective. The phage becomes infective if a starter cell secretes the

CC desired product. Colonies are isolated, and starter cells producing the

CC desired product are selected. The system may be used in metabolic

CC engineering and screening for new activities, and is applicable to a wide

XX variety of starter cell types

SQ Sequence 246 AA;

Query Match 42.7%; Score 47; DB 2; Length 246;

Best Local Similarity 53.3%; Pred. No. 93;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 5 OGIGSTHWYDGVGN 19

Db 11 KGAGTTLWYKSGD 25

RESULT 23

AAW24580

ID AAW24580 standard; protein; 246 AA.

XX

AC AAW24580;

XX

DT 25-MAR-2003 (revised)

DT 11-NOV-1997 (first entry)

XX

DE Modified gpv protein.

XX

KW Lambdaoid bacteriophage; gpv gene; surface protein; phage; hormone; toxin;

KW carbohydrate; lipid; glycoprotein; glycolipid; proteolipid; lipoprotein;

KW lipopolysaccharide; vitamin; terpene; antibiotic; cofactor; enzyme.

XX

OS Synthetic.

XX

PN US5650267-A.

XX

PD 22-JUL-1997.

XX

PF 31-AUG-1994; 94US-00299249.

XX

PR 27-APR-1993; 93US-00053865.

XX

PA (SYMB-) SYMBIOTECH INC.

XX

PI Crea R, Ray BL, Lin ECC;

XX

XX WPI; 1997-384661/35.

DR N-PSDB; AAT80077.

XX

XX New infective lambdaoid bacteriophage constructs - containing a modified

PT gpv gene and a target polypeptide gene, useful for the detection of

PT molecules of interest.

XX

PS Disclosure; Col 15-18; 25pp; English.

XX

CC This sequence represents a modified gpv protein. Removal of up to a third

of the gpv protein of bacteriophage lambda does not affect the assembly or infectivity of the phage. Lambdaoid bacteriophages (LB) having a target molecule linked to the gpv protein can be successfully assembled in vivo, so that the target molecule is displayed on the outer surface of the phage. These genetically modified LB maintain their ability to infect *E. coli*. The gpv protein can be used in the protein construct of the invention. The protein construct comprises a genetically modified gpv protein truncated at its carboxy terminal region, and a target polypeptide (TP) peptide-bonded to the carboxy terminus of the modified gpv protein. The protein construct is used to create an infective LB where the TP is displayed on its outer surface. The LB can be used in methods for detecting and quantifying the presence and amount of a molecule of interest (MOI) in a solution. The methods can be used for detecting MOIs such as proteins, peptides, hormones, enzymes, nucleic acids, carbohydrates, lipids, glycoproteins, glycolipids, proteolipids, lipoproteins, lipopolysaccharides, vitamins, toxins, terpenes, antibiotics, or cofactors. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 246 AA;

Query Match 42.7%; Score 47; DB 2; Length 246;
Best Local Similarity 53.3%; Pred. No. 93;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVGN 19
:|:|:|:|:|:|:
Db 11 KGAGTTLWYKSGSD 25

RESULT 24

AAW22851
ID AAW22851 standard; protein; 246 AA.

AC AAW22851;

DT 16-SEP-1997 (first entry)

DE Fusion protein encoded by conditionally suppressible cistron.

KW Recombinant; lambdaoid; bacteriophage; vector; pV; tail polypeptide;
conditionally suppressible cistron; tail; fusion; protein.

OS Synthetic.

FN US5627024-A.

PD 06-MAY-1997.

PF 05-AUG-1994; 94US-00286888.

PR 05-AUG-1994; 94US-00286888.

PA (SCRI) SCRIPPS RES INST.

PI Brenner S, Maruyama I, Maruyama H;

DR WPI; 1997-271303/24.

PT Recombinant lambdaoid bacteriophage vector - for expression of foreign
protein, especially diagnostic ligand or receptor.

PS Claim 10; Col 63-64; 41pp; English.

CC A novel recombinant lambdaoid bacteriophage vector, comprises a nucleotide
sequence defining the lambdaoid elements for replication and packaging of
the vector into an assembled bacteriophage, and encodes a conditionally
suppressible cistron, for the expression of a tail protein and a fusion
protein, e.g. the present sequence. The vector is useful for producing a
recombinant lambdaoid bacteriophage by infecting an *E. coli* host strain
having a termination codon suppression phenotype with the vector, and
culturing the infected host strain under bacteriophage growth conditions,
especially where the host strain is *E. coli* MCS (ATCC 69674)

SQ Sequence 246 AA;

Query Match 42.7%; Score 47; DB 2; Length 246;
Best Local Similarity 53.3%; Pred. No. 93;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVGN 19
:|:|:|:|:|:|:
Db 11 KGAGTTLWYKSGSD 25

RESULT 25

ABG73548
ID ABG73548 standard; protein; 246 AA.

AC ABG73548;

DT 26-FEB-2003 (first entry)

DE Phage major tail protein pV.

KW Major tail protein; pV; vector; fusion protein.

OS Bacteriophage lambda.

FN US2002110802-A1.

PD 15-AUG-2002.

PF 06-MAY-1997; 97US-00852020.

PR 05-AUG-1994; 94US-00286888.

PA (MARU/) MARUYAMA I.

PA (MARU/) MARUYAMA H.

PA (BREN/) BRENNER S.

PI Maruyama I, Maruyama H, Brenner S;

DR WPI; 2003-090169/08.

PT New recombinant lambdaoid bacteriophage vector having a nucleotide
sequence that defines lambdaoid elements for replication and packaging of
the vector into an assembled bacteriophage, useful for expressing and
detecting proteins.

PS Example; Page 35-36; 45pp; English.

CC This invention describes a novel recombinant lambdaoid bacteriophage
vector comprising a nucleotide sequence that defines the lambdaoid
elements for replication and packaging of the vector into an assembled
bacteriophage, and encodes a conditionally suppressible cistron for
expression of a tail protein and a fusion protein. The fusion protein
comprises: (a) a promoter for transcribing the cistron; (b) a first
upstream translatable sequence that encodes a lambdaoid bacteriophage tail
polypeptide; (c) a first ribosome binding site to initiate translation of
the upstream translatable sequence; (d) a second translatable sequence
operatively lined downstream to the first translatable sequence that
encodes the linker polypeptide in frame with tail polypeptide and
includes a sequence adapted for ligation of an insert polynucleotide that
defines a third translatable sequence downstream from the second
translatable sequence that encodes a preselcted polypeptide; and (e) a
suppressor termination codon within the second translatable sequence that
upon suppression results in read-through to form a fusion polypeptide
consisting of the tail polypeptide, linker polypeptide and preselcted
polypeptide. The vector is useful for expressing a foreign protein on its
surface, which should be more appropriate for proteins that fold in the
cytoplasm, for identifying polypeptides having biological activity, and
for producing and detecting enzymes, lectins, ligands or receptors. This
sequence represents the Bacteriophage lambda pV tail protein used in the
construction of the vector described in the invention

XX Sequence 246 AA;

Query Match 42.7%; Score 47; DB 6; Length 246;
 Best Local Similarity 53.3%; Pred. No. 93;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVN 19
 DB 11 KGAGTTLWYKSGD 25

RESULT 26
 AAW22850
 ID AAW22850 standard; protein; 292 AA.
 XX AC AAW22850;
 XX DT 16-SEP-1997 (first entry)
 XX DE Fusion protein encoded by conditionally suppressible cistron.
 XX KW Recombinant; lambdaoid; bacteriophage; vector; pV; tail polypeptide;
 XX KW conditionally suppressible cistron; tail; fusion; protein.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Peptide 1..176
 FT Misc-difference 177 /note= "pv lambdaoid bacteriophage tail polypeptide"
 FT Region 178..213 /note= "undefined"
 FT Region 178..213 /note= "linker polypeptide"
 US5627024-A.
 06-MAY-1997.
 05-AUG-1994; 94US-00286888.
 05-AUG-1994; 94US-00286888.
 (Scri)) SCRIPPS RES INST.
 Brenner S, Maruyama I, Maruyama H;
 WPI; 1997-271303/24.
 N-PSDB; AAT75445.
 Recombinant lambdaoid bacteriophage vector - for expression of foreign
 protein, especially diagnostic ligand or receptor.
 Claim 3; Col 67-68; 41pp; English.
 A novel recombinant lambdaoid bacteriophage vector, comprises a nucleotide
 sequence defining the lambdaoid elements for replication and packaging of
 the vector into an assembled bacteriophage, and encodes a conditionally
 suppressible cistron, for the expression of a tail protein and a fusion
 protein, e.g. the present sequence. The vector is useful for producing a
 recombinant lambdaoid bacteriophage by infecting an E. coli host strain
 having a termination codon suppression phenotype with the vector, and
 culturing the infected host strain under bacteriophage growth conditions,
 especially where the host strain is E. coli MCS (ATCC 69674)
 Sequence 292 AA;

Query Match 42.7%; Score 47; DB 2; Length 292;
 Best Local Similarity 53.3%; Pred. No. 1.1e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVN 19
 DB 11 KGAGTTLWYKSGD 25

RESULT 27
 ABG73549
 ID ABG73549 standard; protein; 292 AA.
 XX AC ABG73549;
 XX DT 26-FEB-2003 (first entry)
 XX DE Lambda-foo vector fragment SEQ ID 6.
 XX KW Major tail protein; pV; vector; fusion protein; ss.
 XX OS Bacteriophage lambda.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Region 1..176
 FT Misc-difference 177 /note= "pv tail protein region"
 FT Region 178..213 /note= "Xaa represents a suppressor termination codon"
 FT Region 183..203 /note= "lambda-foo region, claimed in claim 8"
 FT Region 183..203 /note= "Pro-Thr linker region"
 US2002110802-A1.
 15-AUG-2002.
 06-MAY-1997; 97US-00852020.
 05-AUG-1994; 94US-00286888.
 (MARU/) MARUYAMA I.
 (MARU/) MARUYAMA H.
 (BREN/) BRENNER S.
 Maruyama I, Maruyama H, Brenner S;
 WPI; 2003-090169/08.
 N-PSDB; ABQ76662.
 New recombinant lambdaoid bacteriophage vector having a nucleotide
 sequence that defines lambdaoid elements for replication and packaging of
 the vector into an assembled bacteriophage, useful for expressing and
 detecting proteins.
 Example; Fig 2; 45pp; English.
 This invention describes a novel recombinant lambdaoid bacteriophage
 vector comprising a nucleotide sequence that defines the lambdaoid
 elements for replication and packaging of the vector into an assembled
 bacteriophage, and encodes a conditionally suppressible cistron for
 expression of a tail protein and a fusion protein. The fusion protein
 comprises: (a) a promoter for transcribing the cistron; (b) a first
 upstream translatable sequence that encodes a lambdaoid bacteriophage tail
 polypeptide; (c) a first ribosome binding site to initiate translation of
 the upstream translatable sequence; (d) a second translatable sequence
 operatively lined downstream to the first translatable sequence that
 encodes the linker polypeptide in frame with tail polypeptide and
 includes a sequence adapted for ligation of an insert polynucleotide that
 defines a third translatable sequence downstream from the second
 translatable sequence that encodes a preselected polypeptide; and (e) a
 suppressor termination codon within the second translatable sequence that
 upon suppression results in read-through to form a fusion polypeptide
 consisting of the tail polypeptide, linker polypeptide and preselected
 polypeptide. The vector is useful for expressing a foreign protein on its
 surface, which should be more appropriate for proteins that fold in the
 cytoplasm, for identifying polypeptides having biological activity, this
 for producing and detecting enzymes, lectins, ligands or receptors. This
 sequence represents a construct containing a truncated lambda V tail
 protein and the vector lambda-foo

XX SQ Sequence 292 AA;

Query Match 42.7%; Score 47; DB 6; Length 292;
 Best Local Similarity 53.3%; Pred. No. 1.1e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
 Db 11 KGAGTTLVYKSGD 25
 :|||:|

RESULT 28

ABR52676
 ID ABR52676 standard; protein; 946 AA.
 XX AC ABR52676;
 XX 20-JUN-2003 (first entry)
 XX Protein sequence #SEQ ID 217.
 XX Multiprotein complex; eukaryote; drug target; diagnosis.
 XX Saccharomyces cerevisiae.
 XX OS
 XX EP1258494-A1.
 XX 20-NOV-2002.
 XX 20-DEC-2001; 2001EP-00130253.
 XX 15-MAY-2001; 2001EP-00111774.
 XX (CELL-) CELLZOME AG.
 XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
 XX Marzioch M, Schultz JD, Superti-Furga GD;
 XX WPI; 2003-250078/25.
 XX N-PSDB; ACC60718.
 XX New isolated protein complexes useful for diagnosing a disease or
 XX disorder, or as a target for an active agent of a pharmaceutical,
 XX preferably a drug target in the treatment or prevention of disease or
 XX disorder.
 XX Disclosure; SEQ ID NO 217; 17pp + Sequence Listing; English.

CC The invention relates to multiprotein complexes from eukaryotes. Proteins
 CC of the invention and DNA sequences encoding them are given in records
 CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
 CC obtainable by using a protein as a bait and isolating the set of proteins
 CC which is attached thereto from cells. Such protein complexes may comprise
 CC up to 30 distinct proteins. Protein complexes of the invention are useful
 CC for diagnosing a disease or disorder, or as a target for an active agent
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for this
 CC patent is not represented in the printed specification, but is based on
 CC sequence information supplied by the European Patent Office. The complete
 CC document is available on CD-ROM

XX SQ Sequence 946 AA;

Query Match 42.7%; Score 47; DB 6; Length 946;
 Best Local Similarity 44.4%; Pred. No. 4e+02;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVG 18
 Db 789 AGAFEAVTSNHWEGGKG 806
 :|||:|

RESULT 29

ABP57428
 ID ABP57428 standard; protein; 946 AA.
 XX AC ABP57428;
 XX 24-APR-2003 (first entry)
 XX Saccharomyces dominant adenine auxotrophic DAD1 protein SEQ ID NO.2.
 XX Saccharomyces cerevisiae; Yeast; dominant adenine auxotrophic; DAD1;
 XX dominant adenine requiring; industrial; microorganism.
 XX OS
 XX WO2003000867-A1.
 XX 03-JAN-2003.
 XX 20-JUN-2002; 2002WO-KR001179.
 XX 21-JUN-2001; 2001KR-00035249.
 XX (SONG/) SONG J.
 XX Song J;
 XX WPI; 2003-184046/18.
 XX N-PSDB; ABZ70970.
 XX Novel pCABIOD101 recombinant vector containing dominant adenine
 XX auxotrophic DAD1 (dominant adenine requiring) gene useful for improving
 XX existing industrial yeast and various microorganisms.

XX Claim 3; Page 23-26; 27pp; English.

CC The present invention describes a pCABIOD101 recombinant vector (KCTC
 CC 1018BP) (I) containing the dominant adenine auxotrophic DAD1 (dominant
 CC adenine requiring) gene (S1, see ABZ70970). Also described: (1) a yeast
 CC transformant (II), Saccharomyces cerevisiae pCABIOD101 constructed by
 CC transforming yeast S. cerevisiae with (I); (2) constructing a dominant
 CC adenine auxotrophic S. cerevisiae 368 strain (KCTC 1018BP), involves
 CC inducing in vitro mutation by treating plasmid pJS8A containing yeast
 CC ADE3 and URA3 genes with hydroxylamine, transforming ade2 ura3 yeasts
 CC with the plasmid pJS82 and culturing the transformants in -Ura plus or
 CC minusAd medium, isolating plasmid DNA from pink or white transformant
 CC colonies containing mutations to the ADE3 gene epistatic to ade2 using
 CC Escherichia coli, and treating the plasmid DNA with restriction enzymes
 CC BamHI and SalI to isolate a DNA fragment containing the mutated ADE3 gene
 CC and transfecting the DNA fragment into yeast strain ade3-130; (3) a
 CC dominant adenine auxotrophic DAD1 gene (III) having a sequence of (S1);
 CC (4) an amino acid sequence having 946 amino acids (present sequence),
 CC encoded by (III); and (5) selecting dominant adenine auxotrophic
 CC transformants containing (I) using tritium suicide enrichment, in which
 CC 3H-sodium formate (3H) is used as tritium in the tritium suicide
 CC enrichment. (I) is useful in improving existing industrial yeast and
 CC various microorganisms. (III) is useful in elucidating roles of its gene
 CC product, C1-tetrahydrofolate synthase in a purine synthesis process, and
 CC its industrial significance and merits are considerable when used in
 CC biological industry

XX SQ Sequence 946 AA;

Query Match 42.7%; Score 47; DB 6; Length 946;
 Best Local Similarity 44.4%; Pred. No. 4e+02;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVG 18
 Db 789 AGAFEAVTSNHWEGGKG 806
 :|||:|

RESULT 30

ADK61804
ID ADK61804 standard; protein; 946 AA.

AC ADK61804;

XX 06-MAY-2004 (first entry)

DT Disease treating protein complex-derived protein #28.

DE protein complex; drug target; diagnosis.

XX Unidentified.

OS Unidentified.

XX EPI338608-A2.

PN EPI338608-A2.

XX 27-AUG-2003.

PD 20-DEC-2002; 2002EP-00102902.

PF 20-DEC-2001; 2001EP-00130253.

XX (CELL-) CELLZONE AG.

PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;

PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;

PI Michon A, Leutwein C, Rick J;

XX WPI; 2003-638460/61.

DR N-PSDB; ADK61805.

XX New screening and protein complexes from eukaryotes, useful as targets in

PT drug screening, or in diagnosing or screening for the presence of a

PT disease or disorder, or a predisposition for developing a disease or

PT disorder in a subject.

XX Disclosure; SEQ ID NO 55; 13pp; English.

PS The invention relates to novel protein complexes comprising a first and a

CC second protein, or its derivative, fragment, homologue or variant. The

CC proteins are selected from given protein complexes, which are not defined

CC in the specification. The variants are encoded by nucleic acids that

CC hybridize to the nucleic acids encoding the proteins under low stringency

CC conditions. The protein complexes are useful as targets for an active

CC agent of a pharmaceutical. These protein complexes are particularly

CC useful as drug targets for the treatment or preventing of a disease or

CC disorder. The complexes and methods above are useful in diagnosing or

CC screening for the presence of a disease or disorder or a predisposition

CC for developing a disease or disorder in a subject. These are also useful

CC in screening for a drug for treatment or prevention of a disease or

CC disorder. The molecule that modulates the amount, activity or protein

CC components of the complex is useful for the manufacture of a medicament

CC for the treatment or prevention of a disease or disorder. This sequence

CC corresponds to a protein of the invention. (Note: the sequence data for

CC this patent did not form part of the printed specification but was

XX obtained from the EPO in electronic format).

XX Sequence 946 AA;

Query Match 42.7%; Score 47; DB 7; Length 946;

Best Local Similarity 44.4%; Pred. No. 4e+02;

Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVG 18

DB 789 AGAFEAFTVSNHWAEGKG 806

RESULT 31

ASU61683

ID ABU61683 standard; protein; 170 AA.

XX ABU61683;

AC ABU61683;

XX

DT 19-AUG-2003 (first entry)

XX Program database protein #2.

XX ERG-like protein 2; ERG-LP2; ERG potassium channel; neuronal cell;

XX muscle cell; potassium channel associated disorder; pain;

XX neurodegenerative disorder; psychiatric disorder; learning disorder;

XX memory disorder; obesity; cardiac disorder; gastrointestinal disorder.

XX Unidentified.

XX US6518398-B1.

XX 11-FEB-2003.

XX 21-JUL-1999; 99US-00358383.

XX 21-JUL-1998; 98US-00119855.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI; 2003-455687/43.

XX New human ERG-like protein (ERG-LP2) potassium channel polypeptide and

XX nucleic acid, useful for treating or diagnosing e.g. Alzheimer's disease,

XX schizophrenia, obesity, restenosis, myocardial infarction, Crohn's

XX disease, pain.

XX Disclosure; Fig 10; 116pp; English.

XX The invention relates to an isolated human ERG-like protein (ERG-LP2) of

CC the ERG potassium channel family and the nucleic acid encoding it. The

CC ERG-LP2 polypeptide or nucleic acid is useful for modulating potassium

CC channel mediated activity in a cell, such as a neuronal cell or a muscle

CC cell. The ERG-LP2 polypeptide or nucleic acid is particularly useful for

CC treating potassium channel associated disorders, e.g. neurodegenerative

CC disorders (e.g. Alzheimer's disease, Parkinson's disease, multiple

CC sclerosis, amyotrophic lateral sclerosis, supranuclear palsy, epilepsy or

CC schizophrenia, Korsakoff's psychosis, mania, anxiety or phobias),

CC learning or memory disorders (e.g. amnesia or age-related memory loss),

CC obesity, cardiac disorders (e.g. arteriosclerosis, ischaemic reperfusion

CC injury, restenosis, congestive heart failure, angina, hypertension,

CC myocardial infarction, coronary artery disease or arrhythmia).

CC gastrointestinal disorders (e.g. atresia, hiatal hernia, peptic ulcers,

CC gastritis, stomach tumours, Crohn's disease or ischaemic bowel disease)

CC or pain (e.g. joint pain, tooth pain or headaches). This sequence

CC represents a protein identified on the program database, which is

CC homologous to a human ERG-like protein 2 (ERG-LP2) domain

XX Sequence 170 AA;

Query Match 42.3%; Score 46.5; DB 6; Length 170;

Best Local Similarity 55.6%; Pred. No. 74;

Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 2 SAFOGIGSTHWYDGVGN 19

DB 11 SKYQFGSDAWVY---GN 25

RESULT 32

ADB66814

ID ADB66814 standard; protein; 170 AA.

XX ADB66814;

XX

XX 04-DEC-2003 (first entry)

XX Potassium channel ERG-LP associated domain, SEQ ID No:27.

XX

KW ERG potassium channel like protein; ERG-LP; tumour; cytostatic.
 OS Unidentified.

XX US2003104429-A1.

XX 05-JUN-2003.

XX 27-JUN-2002; 2002US-00185867.

XX 21-JUL-1998; 98US-00119855.

XX 21-JUL-1999; 99US-00358383.

XX (CURT) CURTIS R A J.

XX Curtis RAJ;

XX WPI; 2003-687835/65.

XX New isolated nucleic acid, useful for producing a polypeptide and
 PT preparing a composition for diagnosing or treating diseases e.g., a
 PT tumor.

XX Disclosure; Page 82; 122pp; English.

XX The present invention relates to novel ERG potassium channel like
 CC proteins, designated ERG-LPs, and the polynucleotide sequences encoding
 CC them. Also disclosed are: a host cell containing the polynucleotide, an
 CC antibody that selectively binds to the polypeptide, a method for
 CC producing the polypeptide, a method for detecting the presence of the
 CC polypeptide or the nucleic acid in a sample, a method for identifying a
 CC compound that binds to the polypeptide, a method for modulating the
 CC activity of the polypeptide, a method for identifying a compound that
 CC modulates the activity of the polypeptide, and a kit. The polynucleotide
 CC sequences are useful for producing the ERG-LP polypeptides. The ERG-LP
 CC polynucleotide and polypeptide sequences are useful for preparing a
 CC composition for diagnosing or treating diseases e.g. tumours. The present
 CC invention is given in the Sequence Listing of the present invention but is
 CC not mentioned elsewhere in the specification.

XX Sequence 170 AA;

Query Match 42.3%; Score 46.5; DB 7; Length 170;
 Best Local Similarity 55.6%; Pred. No. 74;
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 2 SAFQIGSTHWYDGVGN 19

Db 11 SKYQFGSDAWY---GN 25

RESULT 33

AAE10074

ID AAE10074 standard; protein; 35 AA.

XX AAE10074;

XX 29-NOV-2001 (first entry)

XX Human ion channel-35 (ion35) protein.

XX Human; ion channel-35; ion35; antiinflammatory; immunosuppressive;
 KW analgesic; neuroprotective; antidepressant; cardiant;
 KW cytosolic; antiviral; human immunodeficiency virus; HIV; anorectic;
 KW antiviral; thyroid disorder; thyrotoxicosis; myxoedema; renal failure;
 KW Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke;
 KW psychotic disorder; neurological disorder; anxiety; dyskinesia;
 KW Huntington's disease; degenerative disorder; Parkinson's disease;
 KW schizophrenia; Alzheimer's disease; cardiovascular disease; cancer;
 KW metabolic disorder; anorexia; obesity; mental disorder.

XX Homo sapiens.

XX OS

PN WO200168849-A2.

XX 20-SEP-2001.

XX 09-MAR-2001; 2001WO-US007503.

XX 10-MAR-2000; 2000US-0188400P.

XX 10-MAR-2000; 2000US-0188517P.

XX 10-MAR-2000; 2000US-0188518P.

XX 10-MAR-2000; 2000US-0188519P.

XX 05-JUL-2000; 2000US-0215815P.

XX 06-JUL-2000; 2000US-0216481P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Wood LS, Vogeli G, Karnovsky AM, Ruble CL, Linske-O'connell LI;
 PI Wang J, Liu D;

XX WPI; 2001-565795/63.

XX N-PSDB; AAD10074.

XX New ion channel polynucleotides and polypeptides, useful for
 PT identification of ion channel modulators and treatment of mental
 PT disorders, infections, cancer and autoimmune diseases.

XX Claim 31; Page 86; 188pp; English.

XX The patent discloses novel human ion channel polypeptides and their
 CC corresponding polynucleotides. The ion channel sequences and their
 CC modulators are used for the treatment of viral infections (e.g. human
 CC immunodeficiency virus (HIV)), thyroid disorders (e.g., thyrotoxicosis,
 CC myxoedema), renal failure, inflammatory conditions (e.g., Crohn's
 CC disease), rheumatoid arthritis, autoimmune disorders, pain, stroke,
 CC psychotic and neurological disorders (e.g. Huntington's disease), degenerative
 CC schizophrenia), dyskinesias (e.g. Parkinson's disease), cardiovascular
 CC disorders (e.g., Parkinson's disease, Alzheimer's disease), cardio-
 CC vascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity)
 CC and mental disorders. The present sequence is ion channel-35 (ion35)
 CC protein from human

XX Sequence 35 AA;

Query Match 41.8%; Score 46; DB 4; Length 35;
 Best Local Similarity 50.0%; Pred. No. 16;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 7 IGSTHWYDGVGNS 20

Db 4 LGNSHWYDGLSYS 17

RESULT 34

ABU97335

ID ABU97335 standard; peptide; 35 AA.

XX ABU97335;

XX 29-JUL-2003 (first entry)

XX Amino acid sequence for human ion channel cDNA clone Ion35.

XX Human; ion channel; immune response; RFLP; genetic mapping;
 KW restriction fragment length polymorphism; viral infection;
 KW inflammatory condition; Crohn's disease; homeostasis; cancer;
 KW rheumatoid arthritis; autoimmune disorder; CNS disorder; dementia;
 KW central nervous system disorder; Huntington's disease; viricide;
 KW degenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW cardiovascular disease; myocardial infarction; hormonal disorder;
 KW transcription factor; antiinflammatory; antirheumatic; antiarthritic;
 KW immunosuppressive; neurotropic; anticonvulsant; antiparkinsonian;
 KW neuroprotective; cardiant.

XX Homo sapiens.

XX OS

XX		
PV	W02003023014-A2.	
PD	XX	
PF	20-MAR-2003.	
PP	XX	
PR	12-SEP-2002; 2002WO-US029087.	
PS	XX	
PT	12-SEP-2001; 2001US-0318733P.	
PU	13-AUG-2002; 2002US-0403254P.	
PV	XX	
PA	(PHAA) PHARMACIA & UPJOHN CO.	
PI	Roberds SL, Benjamin CW, Karnovsky AM, Ruble CL;	
PL	XX	
PM	WPI; 2003-313250/30.	
PN	DR N-PSDB; ACD01511.	
PO	XX	
PP	Novel human ion channel polypeptide, useful for inducing an immune	
PR	response in a mammal and for treating disease or conditions related to	
PS	central nervous system and cancer.	
PT	XX	
PU	Example 3; Page; 146pp; English.	
PV	XX	
PA	The present invention relates to the isolation of novel human ion channel	
PI	polypeptides, and the polynucleotide sequences encoding them. The human	
PL	ion channel polypeptides are useful for inducing an immune response in a	
PM	mammal, and for identifying a compound which binds to and/or modulates	
PN	the ion channel. The polynucleotide sequences encoding human ion channel	
PO	polypeptides are useful for screening restriction fragment length	
PP	polymorphisms (RFLPs) associated with certain disorders, and for genetic	
PT	mapping. The human ion channel polypeptide and polynucleotide sequences	
PU	are useful in the treatment of diseases or conditions such as viral	
PV	infections, inflammatory conditions (e.g. Crohn's disease), diseases	
PA	related to homeostasis, rheumatoid arthritis, autoimmune disorders,	
PI	central nervous system (CNS) disorders (e.g. dementia, Huntington's	
PL	disease), degenerative disorders (e.g. Parkinson's and Alzheimer's	
PM	disease), cardiovascular diseases (e.g. myocardial infarction), cancer,	
PN	and hormonal disorders. The polynucleotide sequences are useful to design	
PO	novel transcription factors for modulating the expression of human ion	
PP	polypeptides in native cells, and cells transformed or transfected with	
PT	them. The present sequence represents an amino acid sequence encoded by a	
PU	human ion channel cDNA clone	
PV	XX	
PA	Sequence 35 AA;	
PI	Query Match 41.8%; Score 46; DB 6; Length 35;	
PL	Best Local Similarity 50.0%; Pred. No. 16;	
PM	Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;	
PN		
PO	QY 7 IGSTHWYDGVGNS 20	
PP	: : : :	
PT	4 LGNSHYVDGLSYS 17	
PU		
PV		
PA	RESULT 35	
PI	ADE29253	
PL	ID ADE29253 standard; protein; 35 AA.	
PM	XX	
PN	AC ADE29253;	
PO	XX	
PP	DT 29-JAN-2004 (first entry)	
PT	XX	
PU	Novel human ion channel ion-35 protein.	
PV	XX	
PA	nootropic; neuroprotective; neuroleptic; immunosuppressive; cardiant;	
PI	antiartherosclerotic; antiinflammatory; antidepressant; antiarthritic;	
PL	ophthalmologic; cytosstatic; hypertensive; hypotensive; vasotropic;	
PM	antimigraine; analgesic; antiparkinsonian; thrombolytic; antithyroid;	
PN	ion channel; ion-x; brain disorder; mental disorder; schizophrenia;	
PO	depression; anxiety; attention deficit hyperactivity disorder; migraine;	
PP	stroke; neurodegenerative disease; Alzheimer's disease;	
PT	Parkinson's disease; Glaucoma; macular degeneration;	
PU	cardiovascular disease; ischaemia; congestive heart failure; arrhythmia;	
PV	KW	

AC ABG07100;
 DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #7091.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US008631.
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS71287.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 37459; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
 XX sequences. (I) is useful as hybridization probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 126 AA;
 Query Match 41.8%; Score 46; DB 4; Length 126;
 Best Local Similarity 50.0%; Pred. No. 64;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 6 GIGSTHWYDGV 17
 DB 113 GLGASHWAFDTV 124
 RESULT 37
 ADC00916
 ID ADC00916 standard; protein; 247 AA.
 XX
 AC ADC00916;
 XX

DT 04-DEC-2003. (first entry)
 DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 961.
 KW enterohaemorrhagic; anti-bacterial.
 OS Escherichia coli; O157:H7.
 XX JP2002355074-A.
 PN 10-DEC-2002.
 PD 24-JAN-2002; 2002JP-00015959.
 PF 24-JAN-2001; 2001JP-00112010.
 PR (UYTS-) UNIV TSUKUBA.
 PA WPI; 2003-451640/43.
 DR Enterohaemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
 XX and a polypeptide and its use, a polypeptide, a vector and a host cell.
 PT Claim 3; SEQ ID NO 961; 2067pp; Japanese.
 PS The invention relates to a novel enterohaemorrhagic Escherichia coli
 XX O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
 CC has anti-bacterial activity. The polypeptide can be used in detection
 CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
 CC genome of Enterohaemorrhagic E coli O157:H7 was determined. The present
 CC sequence represents an E. coli O157:H7-specific polypeptide of the
 CC invention.
 XX Sequence 247 AA;
 SQ Query Match 41.8%; Score 46; DB 7; Length 247;
 Best Local Similarity 43.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QGIGSTHWYDGVGNS 20
 DB 11 KGAGTTFWMTGNGDA 26
 RESULT 38
 AAR52025
 ID AAR52025 standard; protein; 322 AA.
 XX
 AC AAR52025;
 XX 28-NOV-1994 (first entry)
 DE Bacillus sp. NKS-21 alkali protease.
 XX Bacillus NKS-21 alkali protease; hydrolysis; thermostable enzyme;
 KW detergent stable; washing composition.
 XX Synthetic.
 OS JP06070765-A.
 PN 15-MAR-1994.
 PD 08-OCT-1992; 92JP-00296360.
 PF 10-JUL-1992; 92JP-00207302.
 PR (SHOW) SHOWA DENKO KK.
 PA WPI; 1994-128672/16.
 DR N-PSDB; AAQ61884.
 XX New alkali protease stable to heat and detergent - useful as industrial
 PT

PT enzyme, eg in washing compositions.
 XX
 PS Claim 2; Page 8-9; 10pp; Japanese.
 XX
 CC A novel alkali protease obtained from Bacillus NKS-21 is defined by its
 CC physico-chemical properties including substrate specificity for the
 CC tetrapeptide AAR52024. The enzyme has the amino acid sequence AAR52025
 CC and is stable to heat and detergent making it useful as an industrial
 CC enzyme, e.g. in a washing composition
 XX
 SQ Sequence 322 AA;
 Query Match 41.8%; Score 46; DB 2; Length 322;
 Best Local Similarity 61.5%; Pred. No. 1.8e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QGIGSTHWYDGV 17
 DB 120 QSYGTRKWIEGV 132
 RESULT 39
 AAB36460
 ID AAB36460 standard; protein; 447 AA.
 XX
 AC AAB36460;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Lemon acyl transferase protein SEQ ID NO:22B.
 XX
 KW Strawberry; fruit flavour; biosynthetic pathway; aliphatic; thiolase;
 KW aromatic ester; alcohol acyl transferase; alcohol dehydrogenase;
 KW pyruvate decarboxylase; aminotransferase; esterase; alcohol; aldehyde;
 KW alpha-keto acid; amino acid; fatty acid; acyl-CoA; processed food;
 KW food additive; flavouring; syrup; ice-cream; frozen dessert; yoghurt;
 KW confectionery; flavouring; oral medication; vitamin; aroma; beverage;
 KW alcohol; scent; fragrance; perfume; cosmetic; suspension aid;
 KW aluminum salt; anti-perspirant; pharmaceutical; cleaning product;
 KW insect pheromone; dye carrier; solvent; insect repellent; miticide;
 KW scabicide; plasticiser; deodorant.
 XX
 OS Citrus limon.
 XX
 PN WO200032789-A1.
 XX
 XX 08-JUN-2000.
 PD
 XX
 PF 02-DEC-1999; 99WO-NL000737.
 XX
 XX 02-DEC-1998; 98EP-00204018.
 PR
 PR 12-MAR-1999; 98EP-00200739.
 XX
 XX (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
 PA
 XX Aharoni A, Luecker J, Verhoeven HA, Van Tunen AJ, O'Connell AP;
 PI
 XX WPI; 2000-412335/35.
 DR
 DR N-PSDB; AAC64786.
 XX
 PT A new DNA sequence encoding a polypeptide with alcohol acyl transferase
 PT activity for producing and regulating aromatic and/or aliphatic ester
 PT formation in microorganisms, plant cells or plants.
 XX
 PS Example 5; Page 120-121; 163pp; English.
 XX
 CC The present invention describes nucleotide sequences with thiolase,
 CC alcohol acyl transferase, alcohol dehydrogenase, pyruvate decarboxylase,
 CC aminotransferase and esterase activities, which are involved in the
 CC biosynthetic pathway for aliphatic and/or aromatic ester production in
 CC fruit. The nucleotide sequences can be inserted into the genome of a
 CC fruit-producing plant to regulate aliphatic and/or aromatic ester
 CC formation. Aromatic and/or aliphatic esters in microorganisms, plant

CC cells or plants are produced by inserting thiolase, alcohol acyl
 CC transferase, alcohol dehydrogenase, pyruvate decarboxylase,
 CC aminotransferase and esterase nucleotide sequences into the genome and
 CC feeding the microorganism or plant with alcohol, aldehydes, alpha-keto
 CC acids, or amino acids and fatty acids, and acyl-CoA. The nucleotides and
 CC their proteins can be used in the processed food industry as food
 CC additives to enhance the flavour of syrups, ice-creams, frozen desserts,
 CC yoghurts and confectionery. They are used: as flavouring agents for oral
 CC medications and vitamins; provide flavour and aroma in beverages,
 CC including alcohol; enhance or reduce fruit flavour, aroma, fragrance or
 CC scent; enhance the flavour or aroma of natural, synthetic or artificial
 CC products; for the production of novel combinations of artificial flavour
 CC substances; as antibacterial or anti-fungal agents; as fragrance or
 CC perfumes in cosmetics, creams, sun-protectant products, hair
 CC conditioners, lengthening agents and fixatives in perfumes, suspension
 CC aids for aluminum salts in anti-perspirant pharmaceuticals, cleaning
 CC products, personal care products and animal care products; as insect
 CC disinfectant additives; as degreasing solvents for electronics; as insect
 CC pheromones; and as dye carriers, solvents, insect repellents, miticides,
 CC scabicides, plasticisers and deodorants. The present sequence represents
 CC lemon acyl transferase, from the present invention
 XX
 SQ Sequence 447 AA;
 Query Match 41.8%; Score 46; DB 3; Length 447;
 Best Local Similarity 47.4%; Pred. No. 2.5e+02;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 2 SAFOGIGSTHWYDGVGNS 20
 DB 152 AAALGIGFNHCVDGIGSA 170
 RESULT 40
 AAM00034
 ID AAM00034 standard; protein; 128 AA.
 XX
 AC AAM00034;
 XX
 DT 28-SEP-2001 (first entry)
 XX
 DE Endoxyloglucan transferase sequence #102.
 XX
 KW Moss; carbohydrate metabolism related protein; CMRP; sugar; cofactor;
 KW fine chemical production; carbohydrate; polysaccharide.
 XX
 OS Physcomitrella patens.
 XX
 PN WO200144476-A2.
 XX
 XX 21-JUN-2001.
 PD
 XX 14-DEC-2000; 2000WO-EP012697.
 PF
 XX 16-DEC-1999; 99US-0171101P.
 PR
 XX (BADI) BASF PLANT SCI GMBH.
 PA
 XX Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;
 PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R;
 PI WPI; 2001-398155/42.
 XX
 DR N-PSDB; AAH88720.
 DR
 XX Novel moss nucleic acid molecules encoding a carbohydrate metabolism
 PT related protein useful for modulating production of fine chemicals such
 PT as carbohydrates, cofactors and enzymes from microorganisms and plants.
 XX
 PS Claim 30; Page 115; 133pp; English.
 XX
 CC This invention relates to nucleic acid molecules AAH88708 - AAH88796
 CC isolated from Physcomitrella patens (a moss), which encode carbohydrate
 CC metabolism related proteins (CMRP) represented in AAM00022 - AAM00110.

CC Included in the invention is a vector containing the CMRP cDNA, and a
 CC host cell transformed with the vector. The host cell (a microorganism,
 CC Corynebacterium or Brevibacterium, moss or algae or a plant cell) is
 CC useful for producing a fine chemical such as carbohydrates, cofactors
 CC and/or enzymes. The nucleic acid molecules are suitable for modifying a
 CC carbohydrate production system in a host, e.g., microorganisms and
 CC plants. They are also useful to identify those DNA sequences and enzymes
 CC in other species which are useful to modify the biosynthesis of starch,
 CC cell wall polysaccharides and sugars. The nucleic acid molecules may be
 CC utilised in the genetic engineering of Corynebacterium glutamicum and the
 CC related Brevibacterium species and Acetobacter xylinum and Chlorella to
 CC make it a better or more efficient producer of one or more fine
 CC chemicals. Mutagenesis of one or more CRMPs may also result in CRMPs
 CC having altered activities which indirectly impact the production of one
 CC or more desired fine chemicals from plants. Primers AAH88705 - AAH80707
 CC are used in the sequencing of the CMRP cDNA sequences of the invention
 XX

SQ Sequence 128 AA;

Query Match 41.4%; Score 45.5; DB 4; Length 128;
 Best Local Similarity 42.1%; Pred. No. 77;
 Matches 8; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ASAFQIGISTH-WYDVG 18
 :||: ||| |::|:
 Db 61 SSAYTGMGSKQSWLFGGIG 79

Search completed: July 20, 2005, 17:27:38
 Job time : 99.037 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 17:23:58 ; Search time 44.4444 Seconds
(without alignments)
33.592 Million cell updates/sec

Title: US-10-766-480A-2

Perfect score: 110

Sequence: 1 ASAFQIGSTHWYDGVGNS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	105	95.5	909	US-09-538-092-1315	Sequence 1315, Ap
2	77	70.0	416	US-09-949-016-11669	Sequence 11669, A
3	77	70.0	610	US-09-949-016-6945	Sequence 6945, Ap
4	53	48.2	256	US-09-270-767-46624	Sequence 46624, A
5	49	44.5	497	US-09-252-991A-25136	Sequence 25136, A
6	48	43.6	303	US-09-252-991A-29024	Sequence 29024, A
7	47	42.7	246	US-08-286-888B-1	Sequence 1, Appli
8	47	42.7	246	US-08-294-386C-1	Sequence 1, Appli
9	47	42.7	246	US-08-294-386C-3	Sequence 3, Appli
10	47	42.7	246	US-08-299-249A-1	Sequence 1, Appli
11	47	42.7	246	US-08-299-249A-10	Sequence 10, Appli
12	47	42.7	246	US-08-590-708-1	Sequence 1, Appli
13	47	42.7	246	PCT-US94-06543-1	Sequence 1, Appli
14	47	42.7	246	PCT-US95-10224-1	Sequence 1, Appli
15	47	42.7	246	PCT-US95-10224-3	Sequence 3, Appli
16	47	42.7	292	US-08-286-888B-6	Sequence 6, Appli
17	46.5	42.3	170	US-09-358-383C-27	Sequence 27, Appli
18	45	40.9	344	US-09-902-540-14364	Sequence 14364, A
19	45	40.9	506	US-09-631-594-76	Sequence 76, Appli
20	45	40.9	760	US-08-195-152-2	Sequence 2, Appli
21	45	40.9	760	US-08-754-311B-2	Sequence 2, Appli
22	45	40.9	1279	US-09-489-039A-13602	Sequence 13602, A
23	44	40.0	335	US-09-252-991A-29878	Sequence 29878, A
24	43	39.1	382	US-09-668-097A-8	Sequence 8, Appli
25	43	39.1	475	US-09-252-991A-28111	Sequence 28111, A
26	43	39.1	620	US-09-269-731-6	Sequence 6, Appli
27	43	39.1	620	US-09-988-200-6	Sequence 6, Appli

28 43 39.1 820 3 US-09-313-677-21 Sequence 21, Appli
29 43 39.1 926 3 US-09-313-677-2 Sequence 2, Appli
30 43 39.1 928 1 US-08-474-140-11 Sequence 11, Appli
31 43 39.1 928 1 US-08-477-630-11 Sequence 11, Appli
32 43 39.1 928 1 US-08-472-293-11 Sequence 11, Appli
33 43 39.1 928 1 US-08-474-545-11 Sequence 11, Appli
34 43 39.1 928 2 US-08-478-341-11 Sequence 11, Appli
35 43 39.1 928 3 US-08-996-733-11 Sequence 11, Appli
36 43 39.1 928 3 US-09-514-599-4 Sequence 4, Appli
37 43 39.1 928 4 US-09-996-024-4 Sequence 4, Appli
38 43 39.1 933 3 US-09-313-677-19 Sequence 19, Appli
39 43 39.1 967 3 US-09-313-677-17 Sequence 17, Appli
40 43 1297 4 US-09-107-532A-4552 Sequence 4552, Ap
41 42.5 38.6 334 4 US-09-489-039A-9370 Sequence 9370, Ap
42 42 38.2 63 4 US-09-902-540-11838 Sequence 11838, A
43 42 38.2 297 2 US-09-027-013-3 Sequence 3, Appli
44 42 38.2 297 3 US-09-244-233-3 Sequence 3, Appli
45 42 38.2 455 1 US-08-476-008-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-538-092-1315
; Sequence 1315, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1315
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14028
US-09-538-092-1315

Query Match 95.5%; Score 105; DB 4; Length 909;
Best Local Similarity 90.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASAFQIGSTHWYDGVGNS 20
Db 470 ASAYQGLGSTHWYDGVGNS 489
|||||:|||||
|||||:|||||

RESULT 2

US-09-949-016-11669
; Sequence 11669, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11669
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11669

Query Match      70.0%; Score 77; DB 4; Length 416;
Best Local Similarity 68.4%; Pred. No. 0.0014;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGIGSTHWYDGVGN 19
Db 261 ASNYEGIGTTRWYDGE 279

RESULT 3
US-09-949-016-6945
; Sequence 6945, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6945
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6945

Query Match      70.0%; Score 77; DB 4; Length 610;
Best Local Similarity 68.4%; Pred. No. 0.0022;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGIGSTHWYDGVGN 19
Db 180 ASNYEGIGTTRWYDGE 198

RESULT 4
US-09-270-767-46624
; Sequence 46624, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46624
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46624
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Query Match      48.2%; Score 53; DB 4; Length 256;
Best Local Similarity 44.4%; Pred. No. 3.1;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SAFOGIGSTHWYDGVGN 19
Db 168 SDYQGLGQNRWVFGKG 185

RESULT 5
US-09-252-991A-25136
; Sequence 25136, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25136
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25136

Query Match      44.5%; Score 49; DB 4; Length 497;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 GSTHWYDGVGNS 20
Db 113 GMTYGVYDVGAGNS 125

RESULT 6
US-09-252-991A-29024
; Sequence 29024, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29024
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29024

Query Match      43.6%; Score 48; DB 4; Length 303;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASAFQIGIGSTHWYDGVG 18
Db 198 AAAPFGIGQRHLAGGVG 215

RESULT 7
```


US-08-286-888B-1
; Sequence 1, Application US/08286888B
; Patent No. 5627024
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Ichiro
; APPLICANT: Maruyama, Hiroko
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: LAMBDOID BACTERIOPHAGE VECTORS FOR
; TITLE OF INVENTION: EXPRESSION OF FOREIGN PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5627024th Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,888B
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSI 432.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-286-888B-1

Query Match 42.7%; Score 47; DB 1; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVGN 19
:|:|:|:|:|:
Db 11 KGAGTTLWYKSGD 25

RESULT 8
US-08-294-386C-1
; Sequence 1, Application US/08294386C
; Patent No. 5646030
; GENERAL INFORMATION:
; APPLICANT: Ray, Bryan L.
; APPLICANT: Lin, Edmund C.C.
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: Method Of Isolating Mutant Cells
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,386C
; FILING DATE: August 23, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: SYZZ-010CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/330-1300
; TELEFAX: 617/330-1311
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-294-386C-1
Query Match 42.7%; Score 47; DB 1; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 5 QGIGSTHWYDGVGN 19
:|:|:|:|:|:
Db 11 KGAGTTLWYKSGD 25
RESULT 9
US-08-294-386C-3
; Sequence 3, Application US/08294386C
; Patent No. 5646030
; GENERAL INFORMATION:
; APPLICANT: Ray, Bryan L.
; APPLICANT: Lin, Edmund C.C.
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: Method Of Isolating Mutant Cells
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,386C
; FILING DATE: August 23, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: SYZZ-010CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/330-1300
; TELEFAX: 617/330-1311
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

ANTI-SENSE: NO
US-08-294-386C-3

Query Match 42.7%; Score 47; DB 1; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 OGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYKSGD 25

RESULT 10

US-08-299-249A-1
; Sequence 1, Application US/08299249A
; Patent No. 5650267

GENERAL INFORMATION:
APPLICANT: RAY, Bryan L.; and
APPLICANT: LIN, Edmund C.C.
TITLE OF INVENTION: Method Of Detecting Compounds
TITLE OF INVENTION: Utilizing Genetically Modified
TITLE OF INVENTION: Lambdaoid Bacteriophage
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,249A
FILING DATE: 31-AUG-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,865

FILING DATE: 27-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: SYZ-011FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/526-6000

TELEFAX: 617/526-5000

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: YES

US-08-299-249A-1

Query Match 42.7%; Score 47; DB 1; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 OGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYKSGD 25

RESULT 11

US-299-249A-10

; Sequence 10, Application US/08299249A

; Patent No. 5650267

GENERAL INFORMATION:
APPLICANT: RAY, Bryan L.; and
APPLICANT: LIN, Edmund C.C.
TITLE OF INVENTION: Method Of Detecting Compounds
TITLE OF INVENTION: Utilizing Genetically Modified
TITLE OF INVENTION: Lambdaoid Bacteriophage
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/299,249A

FILING DATE: 31-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,865

FILING DATE: 27-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: SYZ-011FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/526-6000

TELEFAX: 617/526-5000

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 246 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-08-299-249A-10

Query Match 42.7%; Score 47; DB 1; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 OGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYKSGD 25

RESULT 12

US-08-590-708-1

; Sequence 1, Application US/08590708

; Patent No. 5663069

GENERAL INFORMATION:

APPLICANT: RAY, Bryan L.

APPLICANT: LIN, Edmund C.C.

TITLE OF INVENTION: Method Of Detecting

TITLE OF INVENTION: Compounds Utilizing

TITLE OF INVENTION: Chemically Modified

TITLE OF INVENTION: Lambdaoid Bacteriophage

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Allegretti & Witcoff, Ltd.

STREET: 75 State Street

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/590,708
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; CLASSIFICATION: 435
;; APPLICATION NUMBER: US/08/053,866A
;; FILING DATE: 19930427
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kerner, Ann-Louise
;; REGISTRATION NUMBER: 33,523
;; REFERENCE/DOCKET NUMBER: 93,075
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/345-9100
;; TELEFAX: 617/345-9111
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 246 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: YES
;; ANTI-SENSE: NO
;; US-08-590-708-1

Query Match 42.7%; Score 47; DB 1; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWVYKSGD 25

RESULT 13
PCT-US94-06543-1
;; Sequence 1, Application PC/TUS9406543
;; GENERAL INFORMATION:
;; APPLICANT: Ray, Bryan L.
;; TITLE OF INVENTION: Method Of Detecting Compounds
;; TITLE OF INVENTION: Utilizing
;; TITLE OF INVENTION: Genetically Modified Lambdaoid
;; TITLE OF INVENTION: Bacteriophage
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lappin & Kusner
;; STREET: 200 State Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: U.S.A.
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/06543
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kerner, Ann-Louise
;; REGISTRATION NUMBER: 33,523
;; REFERENCE/DOCKET NUMBER: SYZZ-011ECT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/330-1300
;; TELEFAX: 617/330-1311
;; INFORMATION FOR SEQ ID NO: 1:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 246 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: YES
;; ANTI-SENSE: NO
;; PCT-US94-06543-1

Query Match 42.7%; Score 47; DB 5; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWVYKSGD 25

RESULT 14
PCT-US95-10224-1
;; Sequence 1, Application PC/TUS9510224
;; GENERAL INFORMATION:
;; APPLICANT: PRESIDENT AND FELLOWS OF
;; APPLICANT: HARVARD COLLEGE
;; TITLE OF INVENTION: Method Of Isolating Mutant Cells
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lappin & Kusner
;; STREET: 200 State Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: U.S.A.
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/10224
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/294,386
;; FILING DATE: August 23, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kerner, Ann-Louise
;; REGISTRATION NUMBER: 33,523
;; REFERENCE/DOCKET NUMBER: SYZZ-010CIP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/330-1300
;; TELEFAX: 617/330-1311
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 246 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; PCT-US95-10224-1

Query Match 42.7%; Score 47; DB 5; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWVYKSGD 25

RESULT 15
PCT-US95-10224-3
; Sequence 3, Application PC/TUS9510224
; GENERAL INFORMATION:
; APPLICANT: PRESIDENT AND FELLOWS OF
; APPLICANT: HARVARD COLLEGE
; TITLE OF INVENTION: Method Of Isolating Mutant Cells
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/294,386
; FILING DATE: August 23, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: SYZZ-010CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/330-1300
; TELEFAX: 617/330-1311
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-10224-3
Query Match 42.7%; Score 47; DB 5; Length 246;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYKSGD 25
RESULT 16
US-08-286-888B-6
; Sequence 6, Application US/0828688B
; Patent No. 5627024
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Ichiro
; APPLICANT: Maruyama, Hiroko
; TITLE OF INVENTION: LAMBDROID BACTERIOPHAGE VECTORS FOR
; TITLE OF INVENTION: EXPRESSION OF FOREIGN PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5627024th Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,888B
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 432.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 177
; OTHER INFORMATION: /label=Xaa
; OTHER INFORMATION: /note="Wherein Xaa is a suppressor termination
; OTHER INFORMATION: codon"
US-08-286-888B-6
Query Match 42.7%; Score 47; DB 1; Length 292;
Best Local Similarity 53.3%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYKSGD 25
RESULT 17
US-09-358-383C-27
; Sequence 27, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: domain
US-09-358-383C-27
Query Match 42.3%; Score 46.5; DB 4; Length 170;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;
Qy 2 SAFOGIGSTHWYDGVGN 19
Db 11 SKYQFGSDAWVY---GN 25
RESULT 18
US-09-902-540-14364
; Sequence 14364, Application US/09902540

```
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14364
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14364

Query Match 40.9%; Score 45; DB 4; Length 344;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVG 18
Db 175 ANAIDGDPATRWSDGVG 192

RESULT 19
US-09-631-594-76
; Sequence 76, Application US/09631594
; Patent No. 6737237
; GENERAL INFORMATION:
; APPLICANT: MCLEOD, RINA W.
; APPLICANT: ROBERTS, CRAIG W.
; APPLICANT: ROBERTS, FIONA
; APPLICANT: JOHNSON, JENNIFER J.
; APPLICANT: KIRISITS, MICHAEL
; APPLICANT: FERGUSON, DAVID
; APPLICANT: LYONS, RUSSELL
; APPLICANT: MUL, ERNEST
; APPLICANT: MACK, DOUG
; APPLICANT: SAMUEL, BENJAMIN
; APPLICANT: GORNICKI, PIOTR
; APPLICANT: ZUTHER, ELLEN
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
; FILE REFERENCE: 19338-90966
; CURRENT APPLICATION NUMBER: US/09/631,594
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/US00/11478
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US97/12497
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-631-594-76

Query Match 40.9%; Score 45; DB 4; Length 506;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 11 HWYDGVGNS 20
Db 20 HWAYEALGNS 29

RESULT 20
US-08-195-152-2
; Sequence 2, Application US/08195152
; Patent No. 5679541
; GENERAL INFORMATION:
; APPLICANT: Bonini, Nancy M.
; APPLICANT: Leiserson, William M.
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,152
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 760 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-195-152-2

Query Match 40.9%; Score 45; DB 1; Length 760;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 THWYDGVGNS 20
Db 189 SHWTHDGTGSS 199

RESULT 21
US-08-754-311B-2
; Sequence 2, Application US/08754311B
; Patent No. 6623937
; GENERAL INFORMATION:
; APPLICANT: Bonini, Nancy M.
; APPLICANT: Leiserson, William M.
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/754,311B
; FILING DATE: 21-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/195,152
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 760 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-754-311B-2

Query Match 40.9%; Score 45; DB 4; Length 760;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 THWYVDGVNS 20
: || : || : ||
Db 189 SHWTHDGTGSS 199

RESULT 22
US-09-489-039A-13602
; Sequence 13602, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13602
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-13602

Query Match 40.9%; Score 45; DB 4; Length 1279;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 FQIGSTHWYVDGV 17
: || : || : ||
Db 1165 FDSINSTAWIKDV 1178

RESULT 23
US-09-252-991A-29878
; Sequence 29878, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28111
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-28111

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29878
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-29878

Query Match 40.0%; Score 44; DB 4; Length 335;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYVDGV 18
: || : || : ||
Db 297 EDIGTRWVVDVG 310

RESULT 24
US-09-668-097A-8
; Sequence 8, Application US/09668097A
; Patent No. 6673988
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Klein, Ted
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Lipases
; FILE REFERENCE: BB1401 US NA
; CURRENT APPLICATION NUMBER: US/09/668,097A
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/157309
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-09-668-097A-8

Query Match 39.1%; Score 43; DB 4; Length 382;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 STHWYVDGV 17
: || : || : ||
Db 346 STHWSWDGI 354

RESULT 25
US-09-252-991A-28111
; Sequence 28111, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28111
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-28111

```
Query Match      39.1%; Score 43; DB 4; Length 475;
Best Local Similarity 46.7%; Pred. No. 1.9e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      6 GIGSTHWVYDGVGNS 20
DB      214 GLGPLHTTFDGRGNA 228

RESULT 26
US-09-269-731-6
; Sequence 6, Application US/09269731
; Patent No. 633185
; GENERAL INFORMATION:
; APPLICANT: BARBEYRON, Tristan
; APPLICANT: POTIN, Philippe
; APPLICANT: RICHARD, Christophe
; APPLICANT: HENRISSAT, Bernard
; APPLICANT: YVIN, Jean-Claude
; APPLICANT: KLOAREG, Bernard
; TITLE OF INVENTION: Glycolyse hydrolase genes and their
; use for producing enzymes for the biodegradation of
; carrageenans
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
; STREET: 612 Crystal Square 4, 1745 Jefferson Davis
; STREET: Highway
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,731
; FILING DATE: 07-OCT-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/269,731
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 96 12204
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: IRA SCHULTZ
; REGISTRATION NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 412-1155
; TELEFAX: (703) 412-1161
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-269-731-6

Query Match      39.1%; Score 43; DB 3; Length 620;
Best Local Similarity 35.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY      1 ASAFQIGSTHWVYDGVGNS 20
DB      299 ASTFPGVSPAFWMYSTIDRS 318

RESULT 27
US-09-269-731-6
; Sequence 6, Application US/09269731
; Patent No. 633185
; GENERAL INFORMATION:
; APPLICANT: BARBEYRON, Tristan
; APPLICANT: POTIN, Philippe
; APPLICANT: RICHARD, Christophe
; APPLICANT: HENRISSAT, Bernard
; APPLICANT: YVIN, Jean-Claude
; APPLICANT: KLOAREG, Bernard
; TITLE OF INVENTION: Glycolyse hydrolase genes and their
; use for producing enzymes for the biodegradation of
; carrageenans
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
; STREET: 612 Crystal Square 4, 1745 Jefferson Davis
; STREET: Highway
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,731
; FILING DATE: 07-OCT-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR97/01768
; FILING DATE: 06-OCT-1997
; APPLICATION NUMBER: FR 96 12204
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: IRA SCHULTZ
; REGISTRATION NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 412-1155
; TELEFAX: (703) 412-1161
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-269-731-6

Query Match      39.1%; Score 43; DB 3; Length 620;
Best Local Similarity 35.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY      1 ASAFQIGSTHWVYDGVGNS 20
DB      299 ASTFPGVSPAFWMYSTIDRS 318

RESULT 28
US-09-313-677-21
; Sequence 21, Application US/09313677
; Patent No. 6300115
; GENERAL INFORMATION:
; APPLICANT: Teague, W. Martin
; APPLICANT: Brumm, Phillip J.
; APPLICANT: Allen, Larry N.
; APPLICANT: Brikun, Igor A.
; TITLE OF INVENTION: Pullulanase Expression Constructs Containing Alpha
; Amylase Promoter and Leader Sequences
; FILE REFERENCE: Pullulanase Constructs
; CURRENT APPLICATION NUMBER: US/09/313,677
```

; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 60/122,065
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-313-677-21

Query Match 39.1%; Score 43; DB 3; Length 820;
Best Local Similarity 56.2%; Pred. No. 3.4e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 4 FQIGSTHWYDGVGN 19
Db 133 FSYIPSTHAVYDTINN 148

RESULT 29
US-09-313-677-2
; Sequence 2, Application US/09313677
; Patent No. 6300115
; GENERAL INFORMATION:
; APPLICANT: Teague, W. Martin
; APPLICANT: Brumm, Phillip J.
; APPLICANT: Allen, Larry N.
; APPLICANT: Brikun, Igor A.
; TITLE OF INVENTION: Pullulanase Expression Constructs Containing Alpha
; FILE REFERENCE: Pullulanase Constructs
; CURRENT APPLICATION NUMBER: US/09/313,677
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 60/122,065
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Bacillus naganocensis
US-09-313-677-2

Query Match 39.1%; Score 43; DB 3; Length 926;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 4 FQIGSTHWYDGVGN 19
Db 239 FSYIPSTHAVYDTINN 254

RESULT 30
US-08-474-140-11
; Sequence 11, Application US/08474140
; Patent No. 5721127
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE
; APPLICANT: AMORY, ANTOINE
; TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
; TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K Street, N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,140
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-140-11

Query Match 39.1%; Score 43; DB 1; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 4 FQIGSTHWYDGVGN 19
Db 241 FSYIPSTHAVYDTINN 256

RESULT 31
US-08-477-630-11
; Sequence 11, Application US/08477630
; Patent No. 5721128
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE
; APPLICANT: AMORY, ANTOINE
; TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
; TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K Street, N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/477,630
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-42
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-477-630-11

Query Match 39.1%; Score 43; DB 1; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 FQIGSTHWYDGVGN 19
| | | | | : |
DB 241 FSYIPSTHAVYDTINN 256

RESULT 32

US-08-472-293-11
; Sequence 11, Application US/08472293
; Patent No. 5731174
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE
; APPLICANT: AMORY, ANTOINE
; TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
; TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K Street, N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,293
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-1850
; TELEPHAX: (202) 293-1850

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acids
; LENGTH: 928 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-472-293-11

Query Match 39.1%; Score 43; DB 1; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 FQIGSTHWYDGVGN 19
| | | | | : |
DB 241 FSYIPSTHAVYDTINN 256

RESULT 33

US-08-474-545-11
; Sequence 11, Application US/08474545
; Patent No. 5736375
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE
; APPLICANT: AMORY, ANTOINE
; TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
; TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF

; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K Street, N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,545
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-43
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-1850
; TELEPHAX: (202) 293-1850

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-474-545-11

Query Match 39.1%; Score 43; DB 1; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 FQIGSTHWYDGVGN 19
| | | | | : |
DB 241 FSYIPSTHAVYDTINN 256

RESULT 34

US-08-478-341-11
; Sequence 11, Application US/08478341
; Patent No. 5817498
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE
; APPLICANT: AMORY, ANTOINE
; TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
; TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C.
; STREET: 2000 K Street, N.W., Suite 200
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,341
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilhem F. Gadiano, Esq.
; REGISTRATION NUMBER: 37,136
; REFERENCE/DOCKET NUMBER: 4121-45

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-0625
; TELEFAX: (202) 293-1850
; TELEX: 650 383-5605
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-341-11

Query Match          39.1%; Score 43; DB 2; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      4 FQIGSTHWYDGVGN 19
Db      241 FSYIPSTHAVYDTINN 256

RESULT 35
US-08-996-733-11
; Sequence 11, Application US/08996733
; Patent No. 6074854
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE
; APPLICANT: AMORY, ANTOINE
; TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
; TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
; TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 925 Page Mill Road
; CITY: Palo Alto,
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,733
; FILING DATE: 23-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,293
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174,893
; FILING DATE: 28-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09301278
; FILING DATE: 19-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09300744
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09201156
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Debra J. Glaister, Esq.
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC446C1-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 846-7620
; TELEFAX: (650) 845-6504
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acids
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-733-11

Query Match          39.1%; Score 43; DB 3; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      4 FQIGSTHWYDGVGN 19
Db      241 FSYIPSTHAVYDTINN 256

RESULT 36
US-09-514-599-4
; Sequence 4, Application US/09514599
; Patent No. 6350599
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Pullulanase Variants And Methods For
; TITLE OF INVENTION: Preparing Such Variants With Predetermined Properties
; FILE REFERENCE: 6072.200-US
; CURRENT APPLICATION NUMBER: US/09/514,599
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PA 2000 00045
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Bacillus deramificans
US-09-514-599-4

Query Match          39.1%; Score 43; DB 3; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      4 FQIGSTHWYDGVGN 19
Db      241 FSYIPSTHAVYDTINN 256

RESULT 37
US-09-996-024-4
; Sequence 4, Application US/09996024
; Patent No. 6838257
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Pullulanase Variants And Methods For
; TITLE OF INVENTION: Preparing Such Variants With Predetermined Properties
; FILE REFERENCE: 6072.200-US
; CURRENT APPLICATION NUMBER: US/09/996,024
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/514,599
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Bacillus deramificans
US-09-996-024-4

Query Match          39.1%; Score 43; DB 4; Length 928;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      4 FQIGSTHWYDGVGN 19
Db      241 FSYIPSTHAVYDTINN 256
```

RESULT 38

US-09-313-677-19
; Sequence 19, Application US/09313677
; Patent No. 6300115
; GENERAL INFORMATION:
; APPLICANT: Teague, W. Martin
; APPLICANT: Brumm, Phillip J.
; APPLICANT: Allen, Larry N.
; APPLICANT: Brikun, Igor A.
; TITLE OF INVENTION: Pullulanase Expression Constructs Containing Alpha
; FILE REFERENCE: Amylase Promoter and Leader Sequences
; CURRENT APPLICATION NUMBER: US/09/313,677
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 60/122,065
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-313-677-19

Query Match 39.1%; Score 43; DB 3; Length 933;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 FQIGSTHWYDGVGN 19

DB 246 FSYIPSTHAYDTINN 261

RESULT 39

US-09-313-677-17
; Sequence 17, Application US/09313677
; Patent No. 6300115
; GENERAL INFORMATION:
; APPLICANT: Teague, W. Martin
; APPLICANT: Brumm, Phillip J.
; APPLICANT: Allen, Larry N.
; APPLICANT: Brikun, Igor A.
; TITLE OF INVENTION: Pullulanase Expression Constructs Containing Alpha
; FILE REFERENCE: Amylase Promoter and Leader Sequences
; CURRENT APPLICATION NUMBER: US/09/313,677
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 60/122,065
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-313-677-17

Query Match 39.1%; Score 43; DB 3; Length 967;
Best Local Similarity 56.2%; Pred. No. 4.1e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 FQIGSTHWYDGVGN 19

DB 280 FSYIPSTHAYDTINN 295

RESULT 40

US-09-107-532A-4552
; Sequence 4552, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4552:
SEQUENCE CHARACTERISTICS:
LENGTH: 1297 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1297
SEQUENCE DESCRIPTION: SEQ ID NO: 4552:
US-09-107-532A-4552

Query Match 39.1%; Score 43; DB 4; Length 1297;
Best Local Similarity 58.3%; Pred. No. 5.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 STHWYDGVGNS 20

DB 445 ATHWVDGSSNN 456

Search completed: July 20, 2005, 17:33:31
Job time : 45.4444 secs

This Page Blank (uspto)

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 17:31:44 ; Search time 161.481 Seconds
(without alignments)
48.078 Million cell updates/sec

Title: US-10-766-480A-2

Perfect score: 110

Sequence: 1 ASAFQIGSTHWYDGVGNS 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 388188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	77	70.0	809	11	US-09-855-828-1	Sequence 1, Appli
2	77	70.0	809	11	US-09-855-828-13	Sequence 13, Appli
3	50	45.5	39	16	US-10-425-115-270988	Sequence 270988,
4	48	43.6	621	15	US-10-369-493-17047	Sequence 17047, A
5	47	42.7	246	8	US-08-852-020-1	Sequence 1, Appli
6	47	42.7	292	8	US-08-852-020-6	Sequence 6, Appli
7	46.5	42.3	170	14	US-10-185-867-27	Sequence 27, Appli
8	46	41.8	35	10	US-09-802-668-56	Sequence 56, Appli
9	46	41.8	35	14	US-10-243-475-56	Sequence 56, Appli
10	46	41.8	163	16	US-10-437-963-106789	Sequence 106789,
11	45.5	41.4	128	9	US-09-734-569-26	Sequence 26, Appli

12	45.5	41.4	155	15	US-10-424-599-165955	Sequence 155955,
13	45.5	41.4	200	9	US-09-734-569-150	Sequence 150, App
14	45.5	41.4	327	15	US-10-282-122A-73048	Sequence 73048, A
15	45.5	41.4	328	15	US-10-282-122A-75004	Sequence 75004, A
16	45.5	41.4	328	15	US-10-282-122A-75514	Sequence 75514, A
17	45.5	41.4	648	15	US-10-369-493-17192	Sequence 17192, A
18	45	40.9	318	15	US-10-424-599-261644	Sequence 261644,
19	45	40.9	375	16	US-10-437-963-109989	Sequence 109989,
20	45	40.9	488	15	US-10-369-493-18241	Sequence 18241, A
21	45	40.9	506	16	US-10-437-963-165185	Sequence 165185,
22	45	40.9	506	18	US-10-824-194-76	Sequence 76, Appli
23	45	40.9	760	8	US-08-754-311B-2	Sequence 2, Appli
24	45	40.9	970	15	US-10-282-122A-59736	Sequence 59736, A
25	44.5	40.5	106	15	US-10-424-599-284586	Sequence 284586,
26	44.5	40.5	1333	15	US-10-282-122A-55546	Sequence 55546, A
27	44	40.0	146	15	US-10-424-599-143592	Sequence 143592,
28	44	40.0	203	15	US-10-424-599-143593	Sequence 143593,
29	44	40.0	209	9	US-09-738-626-5898	Sequence 5898, Ap
30	44	40.0	332	15	US-10-282-122A-66224	Sequence 66224, A
31	44	40.0	437	15	US-10-424-599-225763	Sequence 225763,
32	44	40.0	437	15	US-10-425-114-51243	Sequence 51243, A
33	44	40.0	491	15	US-10-282-122A-61175	Sequence 61175, A
34	43.5	39.5	116	15	US-10-425-114-41565	Sequence 41565, A
35	43.5	39.5	462	16	US-10-437-963-185820	Sequence 185820,
36	43.5	39.5	955	17	US-10-211-028-108	Sequence 108, App
37	43	39.1	33	16	US-10-425-115-286157	Sequence 286157,
38	43	39.1	58	15	US-10-424-599-206896	Sequence 206896,
39	43	39.1	135	16	US-10-425-115-216910	Sequence 216910,
40	43	39.1	275	9	US-09-925-302-737	Sequence 737, App
41	43	39.1	275	10	US-09-525-302-737	Sequence 737, App
42	43	39.1	320	16	US-10-437-963-170504	Sequence 170504,
43	43	39.1	382	16	US-10-437-963-185346	Sequence 185346,
44	43	39.1	396	15	US-10-282-122A-66898	Sequence 66898, A
45	43	39.1	468	16	US-10-437-963-178033	Sequence 178033,

ALIGNMENTS

RESULT 1
US-09-855-828-1
; Sequence 1, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Crech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human cyclic nucleotide-gated cation channel (CNG)
; OTHER INFORMATION: 3B (CNG3B)
US-09-855-828-1

Query Match 70.0%; Score 77; DB 11; Length 809;
Best Local Similarity 68.4%; Pred. No. 0.017;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVGNS 19

Db 374 ASNYEGIGTTRWYDGVGNS 392

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RESULT 2
US-09-855-828-13
; Sequence 13, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Creesch, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICogen, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CNG3B
US-09-855-828-13

Query Match 70.0%; Score 77; DB 11; Length 809;
Best Local Similarity 68.4%; Pred. No. 0.017; 3; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGN 19
Db 374 ASNTEGIGTTRWYDGEEN 392
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RESULT 3
US-10-425-115-270988
; Sequence 270988, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 270988
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_178738C.1.pap
US-10-425-115-270988

Query Match 45.5%; Score 50; DB 16; Length 39;
Best Local Similarity 53.3%; Pred. No. 6.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 GIGSTHWYDGVGNS 20
Db 11 GKGSTHWLFSWLGS 25
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RESULT 4
US-10-369-493-17047
; Sequence 17047, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17047
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-17047

Query Match 43.6%; Score 48; DB 15; Length 621;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVG 18
Db 388 ATETQGITVTHWITRVG 405
||:||||:||||:|

RESULT 5
US-08-852-020-1
; Sequence 1, Application US/08852020
; Publication No. US20020110802A1
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Ichiro
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: LAMBDROID BACTERIOPHAGE VECTORS FOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 NO. US20020110802A1th Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/852,020
; APPLICATION NUMBER: US/08/852,020
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,888
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 432.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
US-08-852-020-1

Query Match 42.7%; Score 47; DB 8; Length 246;
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Best Local Similarity 53.3%; Pred. No. 1.1e+02; Mismatches 3; Indels 4; Gaps 0;
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYKSGD 25

RESULT 6
US-08-852-020-6
; Sequence 6, Application US/08852020
; Publication No. US20020110802A1
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Ichiro
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESS: Patent Counsel
; STREET: 10666 No. US20020110802A1th Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,020
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,888
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 432.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 177
; OTHER INFORMATION: /label= Xaa
; OTHER INFORMATION: /note= "Wherein Xaa is a suppressor termination
; OTHER INFORMATION: codon"

US-08-852-020-6
Query Match 42.7%; Score 47; DB 8; Length 292;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYKSGD 25

RESULT 7
US-10-185-867-27
; Sequence 27, Application US/10185867
; Publication No. US20030104429A1

; GENERAL INFORMATION:
; APPLICANT: Curtis, RORY A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 27
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: domain
US-10-185-867-27

Query Match 42.3%; Score 46.5; DB 14; Length 170;
Best Local Similarity 55.6%; Pred. No. 89;
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 2 SAPOGIGSTHWYDGVGN 19
Db 11 SKYQFGSDAWY---GN 25

RESULT 8
US-09-802-668-56
; Sequence 56, Application US/09802668
; Publication No. US20030190714A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Vogel, Gabriel
; APPLICANT: Karnovsky, Alla
; APPLICANT: Linske-O'Connell, Lisa I.
; APPLICANT: Wang, Jun
; APPLICANT: Liu, Derong
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00069051
; CURRENT APPLICATION NUMBER: US/09/802,668
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/189,517
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 56
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-668-56

Query Match 41.8%; Score 46; DB 10; Length 35;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 7 IGSTHWYDGVGN 20
Db 4 LGNSHYVDGLSYS 17

RESULT 9
US-10-243-475-56
; Sequence 56, Application US/10243475
; Publication No. US20030194720A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher W.
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels

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; FILE REFERENCE: BHRM0039-100
; CURRENT APPLICATION NUMBER: US/10/243,475
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/403,254
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/318,733
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-475-56

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Query Match          41.8%; Score 46; DB 14; Length 35;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Qy 7 IGSTHWYVDGVGNS 20
    :||:|||||:
Db 4 LGNSHYVDGLSYS 17

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RESULT 10

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US-10-437-963-106789
; Sequence 106789, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

```

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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li Ping

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; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106789
; LENGTH: 163
; TYPE: PRT

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; ORGANISM: Oryza sativa
; FEATURE:

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; OTHER INFORMATION: Clone ID: PAT_MRT4530_11201C.1.pep
US-10-437-963-106789

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Query Match          41.8%; Score 46; DB 16; Length 163;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy 7 IGSTHWYVDGVGNS 20
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Db 1 MGQTHIWDGLGRS 14

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RESULT 11

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US-09-734-569-26
; Sequence 26, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:

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; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reindl, Andreas
; APPLICANT: Cirpus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette

```

```

; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reski, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; TITLE OF INVENTION: in the synthesis of carbohydrates
; FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734,569
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
; SEQ ID NO 26
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-26

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Query Match          41.4%; Score 45.5; DB 9; Length 128;
Best Local Similarity 42.1%; Pred. No. 94;
Matches 8; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

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Qy 1 ASAFQIGIGSTH-WVYDGVG 18
    :||:|||||:
Db 61 SSAYTGMGSKQSWLFGGIG 79

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RESULT 12

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US-10-424-599-165955
; Sequence 165955, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

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```

; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

```

```

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B

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; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165955
; LENGTH: 155
; TYPE: PRT

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; ORGANISM: Glycine max
; FEATURE:

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; OTHER INFORMATION: Clone ID: PAT_MRT3847_120873C.1.pep
US-10-424-599-165955

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Query Match          41.4%; Score 45.5; DB 15; Length 155;
Best Local Similarity 69.2%; Pred. No. 1.e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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Qy 6 GIGSTHW-VYDGV 17
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Db 44 GSGSVHWNVFDGV 56

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RESULT 13

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US-09-734-569-150
; Sequence 150, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:

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```

; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reindl, Andreas
; APPLICANT: Cirpus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke

```



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; APPLICANT: Schmidt, Ralf-Michael
; TITLE OF INVENTION: Reeki, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; FILE REFERENCE: BASF-NAB-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734,569
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
; SEQ ID NO 150
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-150

Query Match      41.4%; Score 45.5; DB 9; Length 200;
Best Local Similarity 42.1%; Pred.No.1.5e+02;
Matches      8; Conservative    6; Mismatches    4; Indels    1; Gaps    1;

QY      1 ASAPQGIGSTH-WVVDGVG 18
        :||: ||:|| |::|::|:|
Db       61 SSAYTGMGSKQSFLFGGIG 79

RESULT 14
US-10-282-122A-73048
; Sequence 73048, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeelbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73048
; LENGTH: 327
; TYPE: PRT

```

```
; Sequence 75514, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75514
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-75514

Query Match 41.4%; Score 45.5; DB 15; Length 328;
Best Local Similarity 28.6%; Pred. No. 2.4e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 17; Gaps 1;

Qy 2 SAFQIGSG-----THWVYDGVGN 19
Db 158 SAFDGLGAKAGDYPPALQSKIDELNGHIYDNNV 192

RESULT 17
US-10-369-493-17192
; Sequence 17192, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
```

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; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17192
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17192

Query Match 41.4%; Score 45.5; DB 15; Length 648;
Best Local Similarity 37.0%; Pred. No. 4.7e+02;
Matches 10; Conservative 4; Mismatches 4; Indels 9; Gaps 1;

Qy 2 SAFQIGSGT-----HMVYDGVGN 19
Db 380 SCLKVGSTGEPWNPPEPWHLFEHVG 406

RESULT 18
US-10-424-599-261644
; Sequence 261644, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 261644
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; NAME/KEY: unsure
; LOCATION: (1)..(318)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_78287C.1.pep
US-10-424-599-261644

Query Match 40.9%; Score 45; DB 15; Length 318;
Best Local Similarity 36.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SAFQIGSGTHWVYDGVGNS 20
Db 150 AAXLGVGINHCICDGGSA 168

RESULT 19
US-10-437-963-109989
; Sequence 109989, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109989
```

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; LENGTH: 375
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14095C.1.pap
US-10-437-109989

Query Match 40.9%; Score 45; DB 16; Length 375;
Best Local Similarity 43.5%; Pred. No. 3.2e+02;
Matches 10; Conservative 6; Mismatches 3; Indels 4; Gaps 2;

QY 1 ASAFOGIGST---HW-VYDVCN 19
DB 55 ADATGLGATTNNWPIYDGLGS 77

RESULT 20
US-10-369-493-18241
; Sequence 18241, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18241
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Thermoplasma acidophilum
US-10-369-493-18241

Query Match 40.9%; Score 45; DB 15; Length 488;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 AFQIGIGSTHWVYDVG 18
DB 335 AFGGLGSPYWDQDARG 350

RESULT 21
US-10-437-963-165185
; Sequence 165185, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165185
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

```

! COUNTRY: United States
! ZIP: 94111-4187
! COMPUTER READABLE FORM:
! MEDIUM TYPE: Floppy disk
! COMPUTER: IBM PC compatible
! OPERATING SYSTEM: PC-DOS/MS-DOS
! SOFTWARE: PatentIn Release #1.0, Version #1.25
! CURRENT APPLICATION DATA:
! APPLICATION NUMBER: US/08/754,311B
! FILING DATE: 21-NOV-1996
! CLASSIFICATION: 435
! PRIOR APPLICATION DATA:
! APPLICATION NUMBER: US 08/195,152
! FILING DATE: 14-FEB-1994
! ATTORNEY/AGENT INFORMATION:
! NAME: Trecartin, Richard F.
! REGISTRATION NUMBER: 31,801
! REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
! TELECOMMUNICATION INFORMATION:
! TELEPHONE: (415) 781-1989
! TELEFAX: (415) 398-3249
! TELEX: 910 277299
! INFORMATION FOR SEQ ID NO: 2:
! SEQUENCE CHARACTERISTICS:
! LENGTH: 760 amino acids
! TYPE: amino acid
! TOPOLOGY: linear
! MOLECULE TYPE: protein
! US-08-754-311B-2

Query Match 40.9%; Score 45; DB 8; Length 760;
Best Local Similarity 54.5%; Pred. No. 6.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 THWYDGVGNS 20
Db 189 SHWTHDGTGS 199

RESULT 24

US-10-282-122A-59736
; Sequence 59736, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

! TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
! FILE REFERENCE: ELITRA.034A
! CURRENT APPLICATION NUMBER: US/10/282,122A
! CURRENT FILING DATE: 2003-02-20
! PRIOR APPLICATION NUMBER: 60/191,078
! PRIOR FILING DATE: 2000-03-21
! PRIOR APPLICATION NUMBER: 60/206,848
! PRIOR FILING DATE: 2000-05-23
! PRIOR APPLICATION NUMBER: 60/207,727
! PRIOR FILING DATE: 2000-05-26
! PRIOR APPLICATION NUMBER: 60/230,335
! PRIOR FILING DATE: 2000-09-06
! PRIOR APPLICATION NUMBER: 60/230,347
! PRIOR FILING DATE: 2000-09-09
! PRIOR APPLICATION NUMBER: 60/242,578
! PRIOR FILING DATE: 2000-10-23
! PRIOR APPLICATION NUMBER: 60/253,625

! PRIOR FILING DATE: 2000-11-27
! PRIOR APPLICATION NUMBER: 60/257,931
! PRIOR FILING DATE: 2000-12-22
! PRIOR APPLICATION NUMBER: 60/267,636
! PRIOR FILING DATE: 2001-02-09
! PRIOR APPLICATION NUMBER: 60/269,308
! PRIOR FILING DATE: 2001-02-16
! Remaining Prior Application data removed - See File Wrapper or PALM.
! NUMBER OF SEQ ID NOS: 78614
! SOFTWARE: PatentIn version 3.1
! SEQ ID NO 59736
! LENGTH: 970
! TYPE: PRT
! ORGANISM: Klebsiella pneumoniae
! US-10-282-122A-59736

Query Match 40.9%; Score 45; DB 15; Length 970;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 PQGIGSTHWYDGV 17
Db 864 FDSINSTAWIKDV 877

RESULT 25

US-10-424-599-284586
; Sequence 284586, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284586
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(106)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99006C.1.pep
! US-10-424-599-284586

Query Match 40.5%; Score 44.5; DB 15; Length 106;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 3 AFQIG-STHWYDGV 16
Db 48 SFQAIGKNPFWYDGV 62

RESULT 26

US-10-282-122A-55546
; Sequence 55546, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

```

Query Match      40.0%; Score 44; DB 15; Length 146;
Best Local Similarity 42.9%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      4 FQGIGSTHWYDGV 17
Db      82 FPGISGLRWYDSI 95

RESULT 28
US-10-424-599-143593
; Sequence 143593, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143593
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100679C.1.pep
US-10-424-599-143593

Query Match      40.0%; Score 44; DB 15; Length 203;
Best Local Similarity 42.9%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      4 FQGIGSTHWYDGV 17
Db      82 FPGISGLRWYDSI 95

RESULT 29
US-09-738-626-5898
; Sequence 5898, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5898
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

```


APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61175
LENGTH: 491
TYPE: PRT
ORGANISM: Legionella pneumophila
US-10-282-122A-61175

Query Match 40.0%; Score 44; DB 15; Length 491;

Best Local Similarity 50.0%; Pred. No. 5.8e+02; DB 15; Length 491;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 SAFOGIGSTHW 13

DB 339 SSFTGLGAPHL 350

RESULT 34

US-10-425-114-41565
Sequence 41565, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 41565
LENGTH: 116
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB189-009-A1_FLI.pep
US-10-425-114-41565

Query Match 39.5%; Score 43.5; DB 15; Length 116;
Best Local Similarity 57.9%; Pred. No. 1.6e+02; DB 15; Length 116;
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 2 SAFOGIGSTHWYDGVGNS 20

DB 64 SHFQTIG-IHWLEDGHFNS 81

RESULT 35

US-10-437-963-185820
Sequence 185820, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 185820
LENGTH: 462
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(462)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_82679C.1.pep
US-10-437-963-185820

Query Match 39.5%; Score 43.5; DB 16; Length 462;

Best Local Similarity 47.6%; Pred. No. 6.5e+02; DB 16; Length 462;
Matches 10; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 ASAFQIGSTHW-VYDGVGNS 20

DB 393 ASHFEPYXSTQWALYDGXADS 413

RESULT 36

US-10-211-028-108
Sequence 108, Application US/10211028
Publication No. US20050027113A1
GENERAL INFORMATION:
APPLICANT: CUBIST PHARMACEUTICALS, INC.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
FILE REFERENCE: CUB-12 PCT CIP
CURRENT APPLICATION NUMBER: US/10/211,028
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: PCT/US02/24310
PRIOR FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: PCT/US01/32354
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/310,385
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 60/379,866
PRIOR FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 108
LENGTH: 955

```
; TYPE: PRT
; ORGANISM: Streptomyces roseosporus
US-10-211-028-108

Query Match      39.5%; Score 43.5; DB 17; Length 955;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 10; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 1 ASAFQIGIST-----HWVVDGUG 18
DB 816 AEGAQIGIGQTAFDTDGVFIEDGAG 840

RESULT 37
US-10-425-115-286157
; Sequence 286157, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286157
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(135)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24075C.1.pep
US-10-425-115-286157

Query Match      39.1%; Score 43; DB 16; Length 33;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 THWVYDGVGN 19
DB 6 THWVFGTGS 15

RESULT 38
US-10-424-599-206896
; Sequence 206896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206896
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28854C.1.pep
US-10-424-599-206896

Query Match      39.1%; Score 43; DB 15; Length 58;
Best Local Similarity 30.0%; Pred. No. 98;
Matches 6; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASAFQIGISTHWVVDGVGNS 20

Query Match      39.1%; Score 43; DB 9; Length 275;
Best Local Similarity 53.3%; Pred. No. 4.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 GIGSTHWVVDGVGNS 20
DB 180 GLQSLHWVYLGLIHS 194

Search completed: July 20, 2005, 17:50:20
Job time : 162.481 secs
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; TYPE: PRT
; ORGANISM: Streptomyces roseosporus
US-10-211-028-108

Query Match      39.5%; Score 43.5; DB 17; Length 955;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 10; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 1 ASAFQIGIST-----HWVVDGUG 18
DB 816 AEGAQIGIGQTAFDTDGVFIEDGAG 840

RESULT 37
US-10-425-115-286157
; Sequence 286157, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286157
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(135)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24075C.1.pep
US-10-425-115-286157

Query Match      39.1%; Score 43; DB 16; Length 33;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 THWVYDGVGN 19
DB 6 THWVFGTGS 15

RESULT 38
US-10-424-599-206896
; Sequence 206896, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206896
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28854C.1.pep
US-10-424-599-206896

Query Match      39.1%; Score 43; DB 15; Length 58;
Best Local Similarity 30.0%; Pred. No. 98;
Matches 6; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ASAFQIGISTHWVVDGVGNS 20

Query Match      39.1%; Score 43; DB 9; Length 275;
Best Local Similarity 53.3%; Pred. No. 4.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 GIGSTHWVVDGVGNS 20
DB 180 GLQSLHWVYLGLIHS 194

Search completed: July 20, 2005, 17:50:20
Job time : 162.481 secs
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; TYPE: PRT
; ORGANISM: Streptomyces roseosporus
US-10-211-028-108

Query Match      39.5%; Score 43.5; DB 17; Length 955;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 10; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

QY 1 ASAFQIGIST-----HWVVDGUG 18
DB 816 AEGAQIGIGQTAFDTDGVFIEDGAG 840

RESULT 37
US-10-425-115-286157
; Sequence 286157, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 216910
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(135)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_129423C.1.pep
US-10-425-115-216910

Query Match      39.1%; Score 43; DB 16; Length 135;
Best Local Similarity 42.9%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASAFQIGIGSTHWVY 14
DB 117 ADAFSGVSSSWWIF 130

RESULT 40
US-09-925-302-737
; Sequence 737, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 737
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: PatentIn Ver. 2.0
US-09-925-302-737

Query Match      39.1%; Score 43; DB 9; Length 275;
Best Local Similarity 53.3%; Pred. No. 4.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 GIGSTHWVVDGVGNS 20
DB 180 GLQSLHWVYLGLIHS 194

Search completed: July 20, 2005, 17:50:20
Job time : 162.481 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 17:20:08 ; Search time 34.8148 Seconds
(without alignments)
55.273 Million cell updates/sec

Title: US-10-766-480A-2

Perfect score: 110

Sequence: 1 ASAFQIGSTHWYDVGNS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	95.5	909	2 S32538	cGMP-gated cation
2	50	45.5	250	2 A90900	hypothetical prote
3	50	45.5	250	2 G85817	hypothetical prote
4	50	45.5	250	2 H90997	hypothetical prote
5	49	44.5	245	2 T13099	major tail protein
6	49	44.5	387	2 B95933	probable calcium-b
7	49	44.5	694	2 A23353	translation elonga
8	48	43.6	246	2 H90833	major tail protein
9	48	43.6	256	2 B85691	probable tail comp
10	48	43.6	621	2 H87662	feruloyl-CoA synth
11	48	43.6	639	2 C95342	nitrous-oxide redu
12	48	43.6	650	2 T44660	nitrous-oxide redu
13	48	43.6	706	2 A55251	cyclic nucleotide-
14	47	42.7	246	1 TLBPVL	major tail protein
15	47	42.7	946	1 A29550	methyltetrahydr
16	46	41.8	247	2 B90733	probable major tai
17	46	41.8	249	2 D85583	probable tail comp
18	46	41.8	323	2 I39867	microbial serine p
19	45.5	41.4	328	2 AG0895	conserved hypotet
20	45.5	41.4	648	2 A83792	acetyl-CoA synthet
21	45	40.9	418	2 AG2872	conserved hypotet
22	45	40.9	420	2 H97648	cinnamoyl ester hy
23	45	40.9	497	2 G95983	probable glycerol
24	45	40.9	752	2 S23818	hypothetical prote
25	45	40.9	760	2 A45174	eye cell developme
26	44.5	40.5	489	2 B97289	lysine-specific pe
27	44	40.0	164	2 T36486	hypothetical prote
28	44	40.0	207	2 B97424	maf protein (maf)
29	44	40.0	207	2 A12641	septum formation a

30 44 40.0 300 2 A87790 protein B0207.6 (i
31 44 40.0 321 2 JC5460 intracellular alka
32 44 40.0 322 2 G83922 intracellular alka
33 44 40.0 332 2 F83533 succinylglutamate
34 44 40.0 471 2 T15394 hypothetical prote
35 44 40.0 709 2 S38241 hypothetical prote
36 44 40.0 808 2 B97303 hypothetical prote
37 43.5 39.5 146 2 T02395 hypothetical prote
38 43.5 39.5 431 2 B81124 conserved hypotet
39 43.5 39.5 431 2 E81900 conserved hypotet
40 43 39.1 37 2 JH0743 Ig heavy chain v r
41 43 39.1 91 2 PL0242 Ig heavy chain v r
42 43 39.1 107 2 PL0240 Ig heavy chain v r
43 43 39.1 107 2 PL0243 Ig heavy chain v r
44 43 39.1 107 2 PL0241 Ig heavy chain v r
45 43 39.1 270 2 JC5603 ES1 protein - zebr

ALIGNMENTS

RESULT 1

S32538

cGMP-gated cation channel 2, rod - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

C:Accession: S32538

R:Chen, T.Y.; Peng, Y.W.; Dhallan, R.S.; Ahamed, B.; Reed, R.R.; Yau, K.W.

Nature 362, 764-767, 1993
A:Title: A new subunit of the cyclic nucleotide-gated cation channel in retinal rods.
A:Reference number: S32538; MUID:93226050; PMID:7682292

A:Accession: S32538

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-909 <CHE>

A:Cross-references: UNIPROT:O43636

C:Keywords: cGMP binding

F:620-742/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 95.5%; Score 105; DB 2; Length 909;

Best Local Similarity 90.0%; Pred. No. 8.6e-08;

Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDVGNS 20

||||:|||||||||||||

Db 470 ASAYQGLGSTHWYDVGNS 489

RESULT 2

A90900

hypothetical protein ECs2169 [imported] - Escherichia coli (strain O157:H7, substrain RIN

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: A90900

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: A90900

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <HAY>

A:Cross-references: UNIPROT:Q9EYD8; GB:BA000007; PIDN:BA035592.1; PID:gl3361635; GSPDB:G

C:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: ECs2169

C:Superfamily: phage lambda major tail protein V

Query Match 45.5%; Score 50; DB 2; Length 250;

Best Local Similarity 50.0%; Pred. No. 4;

Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVGNS 20
:||:||||:|:|:|:
Db 11 KGAGTTLWVYNGKGD 26

RESULT 3

G85817
hypotheical protein Z3087 [imported] - Escherichia coli (strain O157:H7, substrain EDL958)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85817
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85817
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <STO>
A:Cross-references: UNIPROT:Q9EYD8; GB:A8005174; NID:gl2516104; PIDN:AAG57003.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3087
C:Superfamily: phage lambda major tail protein V

Query Match 45.5%; Score 50; DB 2; Length 250;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVGNS 20
:||:||||:|:|:|:
Db 11 KGAGTTLWVYNGKGD 26

RESULT 4

Hypothetical protein ECS2952 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H90997
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90997
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <HAY>
A:Cross-references: UNIPROT:Q9EYD8; GB:BA000007; PIDN:BA836375.1; PID:gl3362421; GSPDB:G
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECS2952
C:Superfamily: phage lambda major tail protein V

Query Match 45.5%; Score 50; DB 2; Length 250;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVGNS 20
:||:||||:|:|:|:
Db 11 KGAGTTLWVYNGKGD 26

RESULT 5

T13099
major tail protein V - phage N15
N:Alternate names: protein gp13
C:Species: phage N15
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13099
R:Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.

submitted to the EMBL Data Library, May 1998

A:Reference number: Z17603
A:Accession: T13099
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-245 <HEN>
A:Cross-references: UNIPROT:O64327; EMBL:AF064539; NID:gl3192683; PID:gl3192697; PIDN:AAC1
C:Genetics:
A:Note: Gene 13
C:Superfamily: phage lambda major tail protein V

Query Match 44.5%; Score 49; DB 2; Length 245;
Best Local Similarity 53.3%; Pred. No. 5.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDGVGN 19
:||:||||:|:|:|:
Db 11 KGAGTTLWVYTGTD 25

RESULT 6

E95933
probable calcium-binding exported protein [imported] - Sinorhizobium meliloti (strain 10;
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95933
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A>Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: E95933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <KUR>
A:Cross-references: UNIPROT:Q92VH1; GB:AL591985; PIDN:CAC49133.1; PID:gl5140618; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB21229
A:Genome: plasmid

Query Match 44.5%; Score 49; DB 2; Length 387;
Best Local Similarity 47.1%; Pred. No. 9.1;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 AFOGIGSTHWYDGVGN 19
:||:||||:|:|:|:
Db 171 ALKQSGNDWVYGGIGN 187

RESULT 7

AG2353
translation elongation factor EF-G [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2353
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2353
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-694 <KUR>
A;Cross-references: UNIPROT:QBYPI9; GB:BA000019; PIDN:BA076082.1; PID:g117133519; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: fus
C;Superfamily: translation elongation factor G; translation elongation factor Tu homolog

Query Match 44.5%; Score 49; DB 2; Length 694;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GIGSTHWYVD 15
Db 659 GVGSFHWAYD 668
|:|:|:|:|:|:|

RESULT 8
H90833
major tail protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90833
R;Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90833
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-246 <HAY>
A;Cross-references: UNIPROT:Q8XGX3; GB:BA000007; PIDN:BA035063.1; PID:g13361104; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECol1640
C;Superfamily: phage lambda major tail protein V

Query Match 43.6%; Score 48; DB 2; Length 246;
Best Local Similarity 53.3%; Pred. No. 7; 9;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYNGNGD 25
|:|:|:|:|:|:|

RESULT 9
B85691
probable tail component of prophage CP-933X Z1894 [imported] - Escherichia coli (strain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85691
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85691
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <STO>
A;Cross-references: UNIPROT:Q8XGX3; GB:AE005174; NID:g12514824; PIDN:AA055990.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1894
C;Superfamily: phage lambda major tail protein V

Query Match 43.6%; Score 48; DB 2; Length 256;
Best Local Similarity 53.3%; Pred. No. 8.2;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGN 19
Db 11 KGAGTTLWYNGNGD 25
|:|:|:|:|:|:|

Db 21 KGAGTTLWYNGNGD 35
RESULT 10
H87662
feruloyl-CoA synthetase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87662
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.
n, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-621 <STO>
A;Cross-references: UNIPROT:Q9A368; GB:AE005673; NID:g13425038; PIDN:AAK25300.1; GSPDB:G
C;Genetics:
A;Gene: CC3338

Query Match 43.6%; Score 48; DB 2; Length 621;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVG 18
Db 388 ATETQGITVTHWITERVG 405
|:|:|:|:|:|:|

RESULT 11
C95342
nitrous-oxide reductase (EC 1.7.99.6) NosZ [imported] - Sinorhizobium meliloti (strain 1
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95342
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-639 <KUR>
A;Cross-references: UNIPROT:Q59746; GB:AE006469; PIDN:AAK65301.1; PID:g14523756; GSPDB:G
A;Experimental source: strain 1021, mesoplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, A.; Barloy-Hubler, F.;
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: nosZ
A;Gene: nosZ
C;Superfamily: nitrous-oxide reductase
C;Keywords: oxidoreductase

Query Match 43.6%; Score 48; DB 2; Length 639;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGNS 20
Db 376 GLGPLHTAYDKGNA 390
|:|:|:|:|:|:|

RESULT 12

T44660
nitrous-oxide reductase (EC 1.7.99.6) [imported] - Bradyrhizobium japonicum
C:Species: Bradyrhizobium japonicum
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44660
R:Bedmar, E.J.; Velasco, L.; Xu, C.A.; Delgado, M.J.
submitted to the EMBL Data Library, March 1998
A:Description: Bradyrhizobium japonicum nosRZDFYLX gene cluster.
A:Reference number: Z22825
A:Accession: T44660
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-650 <BED>
A:Cross-references: UNIPROT:Q89XJ6; EMBL:AJ002531; PIDN:CAA05518.1
A:Experimental source: strain USDA110
C:Genetics:
A:Gene: nosZ
C:Superfamily: nitrous-oxide reductase
C:Keywords: oxidoreductase

Query Match 43.6%; Score 48; DB 2; Length 650;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 GIGSTHWVYDGVNS 20

DB 387 GLGPLHTAYDGKNA 401

RESULT 13

A55251
cyclic nucleotide-gated Ca++ channel protein CNG-3 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55251; S43976
R:Bel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockerzi, V.
Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994
A:Title: Another member of the cyclic nucleotide-gated channel family, expressed in testis
A:Reference number: A55251; MUID:94224768; PMID:8170936
A:Accession: A55251
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-706 <BIB>
A:Cross-references: UNIPROT:Q29441; GB:X76485; NID:9488728; PIDN:CAA54023.1; PID:9488729
A:Experimental source: kidney
R:Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.; Nature 368, 859-863, 1994
A:Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from man
A:Reference number: S43976; MUID:94211295; PMID:7512693
A:Accession: S43976
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-706 <WEY>
A:Cross-references: GB:X89600; NID:908823; PIDN:CAA61759.1; PID:9088824
A:Experimental source: testis
C:Genetics:
A:Gene: CNG3

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cGMP binding; ion channel; ion transport; membrane protein
F:501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 43.6%; Score 48; DB 2; Length 706;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 SAFOGISTHWVYDGVN 19

DB 344 SKFIGFTDSWVYPVNSN 361

RESULT 14

TLBPVL

major tail protein V - phage lambda

C:Species: Phage lambda
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: D43008; B43014; A04359
R:Daniels, D.
submitted to the Nucleic Acid Sequence Database, September 1982
A:Reference number: A94614
A:Accession: D43008
A:Molecule type: DNA
A:Residues: 1-246 <DAN>
A:Cross-references: UNIPROT:P03733
R:Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.
J. Mol. Biol. 162, 729-773, 1982
A:Title: Nucleotide sequence of bacteriophage lambda DNA.
A:Reference number: A92891; MUID:83189071; PMID:6221115
A:Accession: B43014
A:Molecule type: DNA
A:Residues: 1-246 <SAN>
A:Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:9215104; I
C:Comment: Gene V protein is the major component of the tail. It makes up the tubular po
r mature phage.
C:Genetics:
A:Gene: V
A:Map position: 18.46-19.98
C:Superfamily: phage lambda major tail protein V

Query Match 42.7%; Score 47; DB 1; Length 246;
Best Local Similarity 53.3%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWVYDGVN 19

DB 11 KGAGTTLWVYKSGD 25

RESULT 15

A29550
methylenetetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) - yeast (Saccharomyces cerevi
N:Alternate names: C1-tetrahydrofolate synthase; protein YGR204w
N:Contents: format-tetrahydrofolate ligase (EC 6.3.4.3); methylenetetrahydrofolate cyclo
C:Species: Saccharomyces cerevisiae
C:Date: 21-May-1988 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A29550; S53927; S64526; S63853
R:Staben, C.; Rabinowitz, J.C.
J. Biol. Chem. 261, 4629-4637, 1986
A:Title: Nucleotide sequence of the Saccharomyces cerevisiae ADE3 gene encoding C1-tetra
A:Reference number: A92580; MUID:86168166; PMID:3514599
A:Accession: A29550
A:Molecule type: DNA
A:Residues: 1-946 <STA>
A:Cross-references: UNIPROT:P07245; EMBL:M12878; NID:gl71004; PIDN:AAA66316.1; PID:gl7100
R:Guerrero, P.; Barreiros, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousac
submitted to the EMBL Data Library, April 1995
A:Description: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII
es, of the human.
A:Reference number: S53922
A:Accession: S53927
A:Molecule type: DNA
A:Residues: 1-946 <GUE>
A:Cross-references: EMBL:Z49133; NID:g790489; PIDN:CAA88997.1; PID:g790495
A:Experimental source: strain S228C
R:Guerrero, P.; Barreiros, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pousac
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64517
A:Accession: S64526
A:Molecule type: DNA
A:Residues: 1-946 <GUM>
A:Cross-references: EMBL:Z72989; NID:gl323364; PIDN:CAA97231.1; PID:gl323365; GSPDB:GN00C
A:Experimental source: strain S288C
R:Guerrero, P.; Barreiros, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousac
Yeast 12, 273-280, 1996
A:Title: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII reveals
terial electron-transferring flavoproteins (beta-chain) and of the Escherichia coli phosph

Db 158 SAFDGLGAKAGDYPPALQSKIDELNGWIYDNVNN 192

RESULT 20
AB3792
acetyl-CoA synthetase BH1137 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: AB3792
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: AB3792
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-648 <STO>
A:Cross-references: UNIPROT:Q9KDS4; GB:AP001511; GB:BA000004; NID:gi10173727; PIDN:BA048
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1137
C:Superfamily: acetate-CoA ligase; acetate-CoA ligase homology

Query Match 41.4%; Score 45.5; DB 2; Length 648;
Best Local Similarity 37.0%; Pred. No. 54;
Matches 10; Conservative 4; Mismatches 4; Indels 9; Gaps 1;

Qy 2 SAFQIGIST-----HWYDGVGN 19
| : |||||
| : |||||
380 SCLKVIKIGTGPWNPPEPHWHLFEHVG 406
| : |||||
| : |||||

Db 380 SCLKVIKIGTGPWNPPEPHWHLFEHVG 406

RESULT 21
AG2872
conserved hypothetical protein Atu2409 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG2872
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tsao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
sler, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2872
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <KUR>
A:Cross-references: UNIPROT:Q8UCS4; GB:AE008688; PIDN:AAL43397.1; PID:gi17740895; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2409
A:Map position: circular chromosome

Query Match 40.9%; Score 45; DB 2; Length 418;
Best Local Similarity 43.8%; Pred. No. 40;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASAFQIGISTHWYDVG 16
| : ||||| : |||||
| : ||||| : |||||
234 ANPYQGGKSYWQYSG 249
| : ||||| : |||||
| : ||||| : |||||

Db 234 ANPYQGGKSYWQYSG 249

RESULT 22
H37648
cinnamoyl ester hydrolase esta (AF164516) [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: H97648
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.

Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: H97648
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KUR>
A:Cross-references: UNIPROT:Q8UCS4; GB:AE007869; PIDN:AAK88145.1; PID:gl5157583; GSPDB:G
C:Genetics:
A:Gene: AGR C 4370
A:Map position: circular chromosome

Query Match 40.9%; Score 45; DB 2; Length 420;
Best Local Similarity 43.8%; Pred. No. 40;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASAFQIGISTHWYDVG 16
| : ||||| : |||||
| : ||||| : |||||
236 ANPYQGGKSYWQYSG 251
| : ||||| : |||||
| : ||||| : |||||

Db 236 ANPYQGGKSYWQYSG 251

RESULT 23
G95983
probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95983
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95983
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <KUR>
A:Cross-references: UNIPROT:O86033; GB:AL591985; PIDN:CAC49535.1; PID:gl5141022; GSPDB:G
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: glpK; Smb21009
A:Genome: plasmid
C:Superfamily: xylulokinase
C:Keywords: phosphotransferase

Query Match 40.9%; Score 45; DB 2; Length 497;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 APOGIGSTHWYDGVG 18
| : ||||| : |||||
| : ||||| : |||||
345 AFTGLGAPHWDPDARG 360
| : ||||| : |||||
| : ||||| : |||||

Db 345 AFTGLGAPHWDPDARG 360

RESULT 24
S23818
hypothetical protein Tnp2 - garden snapdragon transposable element Tam1
C:Species: Antirrhinum majus (garden snapdragon)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S23818; S18551
R:Nacken, W.K.F.; Piotrowiak, R.; Siedler, H.; Sommer, H.
submitted to the EMBL Data Library, January 1991
A:Description: The transposable element TAM1 from Antirrhinum majus shows structural hom
A:Reference number: S23817
A:Accession: S23818
A:Molecule type: DNA

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
Article: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:21608550; PMID:11743193
A;Accession: A12641
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-207 <KUP>
A;Cross-references: UNIPROT:Q8UHX5; GB:AE008688; PIDN:AAL41551.1; PID:gl7738884; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: maf
A;Map position: circular chromosome
C;Superfamily: septum formation protein maf

Query Match 40.0%; Score 44; DB 2; Length 207;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GSTHWVYDGV 17
Db 108 GRSHVYTG 117

RESULT 30
A87790
protein B0207.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A87790
C;anonymus, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; PMID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A87790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <STO>
A;Cross-references: UNIPROT:O01426; GB:chr_1; PIDN:AAB52461.1; PID:gl943807; GSPDB:GN000
C;Genetics:
A;Note: weak similarity to ATPases
A;Gene: B0207.6
A;Map position: 1

Query Match 40.0%; Score 44; DB 2; Length 300;
Best Local Similarity 53.8%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 QGIGSTHWVYDGV 17
Db 24 ENLGSTHWYMGV 36

RESULT 31
JC5460
intracellular alkaline serine proteinase (SC 3.4.-.-) - Thermoactinomyces sp.
C;Species: Thermoactinomyces sp.
C;Date: 17-Jun-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5460; PC4328
R;Tsuchiya, K.; Ikeda, I.; Tsuchiya, T.; Kimura, T.
Biosci. Biotechnol. Biochem. 61, 298-303, 1997
A;Title: Cloning and expression of an intracellular alkaline protease gene from alkaloph
A;Reference number: JC5460; PMID:97212029; PMID:9058969
A;Accession: JC5460
A;Molecule type: DNA
A;Residues: 1-321 <TSUL>
A;Cross-references: UNIPROT:P74937; DDBJ:D87557; NID:gl5136872; PIDN:BAI13418.1; PID:gl513

A;Experimental source: strain HS682
A;Accession: PC4328
A;Molecule type: protein
A;Residues: 16-45 <TSU2>
C;Superfamily: Bacillus intracellular serine proteinase; subtilisin homology
C;Keywords: hydrolase
F;16-321/Product: intracellular alkaline serine proteinase #status predicted <MAT>
F;40-263/Domain: subtilisin homology <SBT>
F;32,86,220/Active site: Asp, His, Ser #status predicted

Query Match 40.0%; Score 44; DB 2; Length 321;
Best Local Similarity 46.2%; Pred. No. 42;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QGIGSTHWVYDGV 17
Db 120 RGFGTTEWVVEGI 132

RESULT 32
G83922
intracellular alkaline serine proteinase isp [imported] - Bacillus halodurans (strain C-1
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83922
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; PMID:20512582; PMID:11058132
A;Accession: G83922
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-322 <STO>
A;Cross-references: UNIPROT:Q9KAV3; GB:AP001514; GB:BA000004; NID:gi0174613; PIDN:BA00590
C;Genetics:
A;Gene: isp
C;Superfamily: Bacillus intracellular serine proteinase; subtilisin homology

Query Match 40.0%; Score 44; DB 2; Length 322;
Best Local Similarity 46.2%; Pred. No. 42;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QGIGSTHWVYDGV 17
Db 121 RGFGTTEWVVEGI 133

RESULT 33
F83533
succinylglutamate desuccinylase PA0901 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83533
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; PMID:20437337; PMID:10984043
A;Accession: F83533
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <STO>
A;Cross-references: UNIPROT:O50177; GB:AE004524; GB:AE004091; NID:g9946795; PIDN:AAG04290
C;Genetics:
A;Experimental source: strain PA01
C;Superfamily: Yersinia pestis hypothetical protein aruE

Query Match 40.0%; Score 44; DB 2; Length 332;
Best Local Similarity 57.1%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
QY 5 QGIGSTHWYDVG 18
Db 294 EDIGGTRWVDEVG 307

RESULT 34
T15394
hypothetical protein C03F11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15394
R:Bentley, D.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C03F11.
A:Reference number: Z18342
A:Accession: T15394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-471 <BEN>
A:Cross-references: UNIPROT:Q11122; EMBL:U39744; NID:g1049465; PID:g1049466; PIDN:AAA804
C:Genetics:
A:Gene: CESP:C03F11.1
A:Introns: 21/1; 47/2; 71/2; 137/3; 174/1; 234/3; 336/3; 415/2

Query Match 40.0%; Score 44; DB 2; Length 471;
Best Local Similarity 46.2%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASAPOGIGSTHW 13
Db 97 AEKFGVSKTHWI 109

RESULT 35
S38241
hypothetical protein - Coxiella burnetii
C:Species: Coxiella burnetii
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S38241
R:Thiele, D.; Willens, H.; Haas, M.; Krause, H.
submitted to the EMBL Data Library, October 1993
A:Reference number: S38215
A:Accession: S38241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-709 <THI>
A:Cross-references: UNIPROT:Q45948; EMBL:X75356; NID:g407370; PIDN:CAA53129.1; PID:g4073

Query Match 40.0%; Score 44; DB 2; Length 709;
Best Local Similarity 63.6%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 GSTHWYDVG 18
Db 263 GSAHYEYDGLG 273

RESULT 36
B97303
hypothetical protein CAC3279 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97303
R:Nolling, J.; Bretton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97303
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-808 <KUR>

A:Cross-references: UNIPROT:Q97E37; GB:AE001437; PIDN:AAK81213.1; PID:g15026356; GSPDB:GH
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3279

Query Match 40.0%; Score 44; DB 2; Length 808;
Best Local Similarity 66.7%; Pred. No. 116+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 QGIGSTHWYDVG 16
Db 314 QNIGQDWWYDVG 325

RESULT 37
T02395
hypothetical protein At2g44400 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F411.21
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02395; A84878
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
A:Reference number: Z14667
A:Accession: T02395
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-146 <ROU>
A:Cross-references: UNIPROT:O64874; EMBL:AC004521; NID:g3128166; PID:g3128182
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84878
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <STO>
A:Cross-references: GB:AE002093; NID:g3128182; PIDN:AAC16086.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g44400; F411.21
A:Map position: 2

Query Match 39.5%; Score 43.5; DB 2; Length 146;
Best Local Similarity 47.4%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 1 ASAFQ----GIGSTHWY 14
Db 116 ASSFQCCVCRGLGSNWLY 134

RESULT 38
B81124
conserved hypothetical protein NMB1096 [imported] - Neisseria meningitidis (strain MCS8
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81124
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiagnani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: B81124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-431 <TET>
A:Cross-references: UNIPROT:Q9UZE1; GB:AE002459; PIDN:g7226320; NID:g7226320; PIDN:AAF4148
```

A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1096

Query Match 39.5%; Score 43.5; DB 2; Length 431;
Best Local Similarity 36.0%; Pred. No. 69;
Matches 9; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

QY 1 ASAFQGI-----GSTHWYDGVGNS 20
DB 127 AGQYQGYMANIDARPYWYDAVGDS 151

RESULT 39

E81900
Hypothetical protein NMA1315 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: E81900
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-431 <PAR>
A;Cross-references: UNIPROT:Q9JUH0; GB:ALJ162755; GB:ALJ157959; NID:g7379742; PIDN:CAB8456
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1315

Query Match 39.5%; Score 43.5; DB 2; Length 431;
Best Local Similarity 36.0%; Pred. No. 69;
Matches 9; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

QY 1 ASAFQGI-----GSTHWYDGVGNS 20
DB 127 AGQYQGYMANIDARPYWYDAVGDS 151

RESULT 40

JH0743
Ig heavy chain V region (clone B17-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: JH0743
R;Jacob, J.; Kelsoe, G.
J. Exp. Med. 176, 679-687, 1992
A;Title: In situ studies of the primary immune response to (4-hydroxy-3-nitrophenyl)aceb
A;Reference number: JH0721; MUID:92381435; PMID:1512536
A;Accession: JH0743
A;Molecule type: DNA
A;Residues: 1-37 <JAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 39.1%; Score 43; DB 2; Length 37;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 HWVDGVGN 19
DB 8 HWVFEVGN 16

Search completed: July 20, 2005, 17:32:25
Job time : 35.8148 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 17:19:48 ; Search time 170.37 Seconds
(without alignments)
60.114 Million cell updates/sec

Title: US-10-766-480A-2

Perfect score: 110
Sequence: 1 ASAFQIGSTHWYDGVGNS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	100.0	147	2 Q9QWK1	Q9QWK1 rattus norv
2	110	100.0	858	2 O55157	O55157 rattus norv
3	110	100.0	866	2 O80XL8	O80XL8 mus musculus
4	110	100.0	1339	2 O35788	O35788 rattus norv
5	105	95.5	909	1 CNQ4_HUMAN	Q14028 homo sapien
6	105	95.5	1245	2 O43636	O43636 homo sapien
7	105	95.5	1251	2 Q9UMG2	Q9UMG2 homo sapien
8	102	92.7	938	2 O77658	O77658 bos taurus
9	102	92.7	948	2 O77659	O77659 bos taurus
10	102	92.7	952	2 O77660	O77660 bos taurus
11	102	92.7	1394	1 CNQ4_BOVIN	Q28181 bos taurus
12	77	70.0	809	1 CNB3_HUMAN	Q9NQW8 homo sapien
13	74	67.3	694	1 CNB3_MOUSE	Q91J29 m cyclic-nu
14	74	67.3	782	1 CNB3_CANFA	O8NID7 canis famil
15	53	48.2	515	2 Q95SL0	Q95SL0 drosophila
16	53	48.2	1040	2 Q9W2D5	Q9W2D5 drosophila
17	52	47.3	312	2 Q38230	Q38230 lactococcus
18	52	47.3	333	2 Q858B2	Q858B2 lactococcus
19	51	46.4	375	2 O845F2	O845F2 uncultured
20	50	45.5	226	2 O84XQ4	O84XQ4 solanum tub
21	50	45.5	250	2 O687F6	O687F6 bacterioph
22	50	45.5	250	2 O9EYD8	O9EYD8 escherichia
23	49	44.5	54	2 O8FI67	O8FI67 escherichia
24	49	44.5	188	2 O64UF8	O64UF8 bacterioides
25	49	44.5	245	2 O64327	O64327 bacterioides
26	49	44.5	256	2 O8FEW5	O8FEW5 escherichia
27	49	44.5	375	2 O845F4	O845F4 uncultured
28	49	44.5	387	2 Q9ZVH1	Q9ZVH1 rhizobium m
29	49	44.5	694	2 Q8YF19	Q8YF19 anabaena sp
30	49	44.5	968	1 CITC_DROME	O96553 d c-1-tetra
31	48	43.6	246	2 Q7AEY8	Q7AEY8 escherichia

32	48	43.6	256	2 Q8X6X3	Q8X6X3 escherichia
33	48	43.6	374	2 Q845F3	Q845F3 uncultured
34	48	43.6	374	2 Q845F7	Q845F7 uncultured
35	48	43.6	375	2 Q845D4	Q845D4 uncultured
36	48	43.6	375	2 Q845D9	Q845D9 uncultured
37	48	43.6	375	2 Q845E6	Q845E6 uncultured
38	48	43.6	375	2 Q845F8	Q845F8 uncultured
39	48	43.6	375	2 Q845G0	Q845G0 uncultured
40	48	43.6	375	2 Q845G1	Q845G1 uncultured
41	48	43.6	375	2 Q845G2	Q845G2 uncultured
42	48	43.6	375	2 Q845G4	Q845G4 uncultured
43	48	43.6	375	2 Q845G6	Q845G6 uncultured
44	48	43.6	375	2 Q845G8	Q845G8 uncultured
45	48	43.6	375	2 Q845H1	Q845H1 uncultured

ALIGNMENTS

RESULT 1

Q9QWK1 PRELIMINARY; PRT; 147 AA.
AC Q9QWK1.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Cyclic nucleotide-gated cation channel alpha subunit (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Qiu W., Guggino S.E.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015728; AAC16405.1; -;
FT NON TER 1
FT NON TER 147
SQ SEQUENCE 147 AA; 17023 MW; 5DAACB35C6A8A603 CRC64;

Query Match 100.0%; Score 110; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVGNS 20

Db 39 ASAFQIGSTHWYDGVGNS 58

RESULT 2

O55157 PRELIMINARY; PRT; 858 AA.
AC O55157.
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclic nucleotide-gated cation channel beta subunit (Cyclic
nucleotide-gated channel beta subunit 1b).
GN Name=CNQ4.3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Olfactory epithelium;
RX MEDLINE=98208604; PubMed=9539801; DOI=10.1073/pnas.95.8.4696;
RA Sautter A., Zong X., Hofmann F., Biel M.;
RT "An isoform of the rod photoreceptor cyclic nucleotide-gated channel
beta subunit expressed in olfactory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:4696-4701(1998).
RN [2]
RP SEQUENCE FROM N.A.

```
RX MEDLINE=99307326; PubMed=10377344;
RA Bonick W., Bradley J., Muller F., Sesti F., Boekhoff I., Ronnett G.V.,
RA Kaupp U.B., Frings S.;
RT "The native rat olfactory cyclic nucleotide-gated channel is composed
RT of three distinct subunits.";
RL J. Neurosci. 19:5332-5347(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Boenigk W., Sesti F., Bradley J., Ronnett G., Mueller F., Kaupp U.B.,
RA Frings S.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ000515; CAA04152.1; -.
DR EMBL; AF068572; AAC19120.1; -.
DR HSSP; O88703; IQ43.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; F: ion channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR InterPro; IPR00595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR Pfam; PF00027; cNMP binding; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00442; CNMP_BINDING_3; 1.
DR PROSITE; PS0042; CNMP_BINDING_3; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 858 AA; 96358 MW; 10B07CC41119F9A4 CRC64;

Query Match 100.0%; Score 110; DB 2; Length 858;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGNS 20
Db |||||
427 ASAFQIGSTHWYDGVGNS 446

RESULT 3
ID Q80XL8 PRELIMINARY; PRT; 866 AA.
AC Q80XL8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cngb1b protein (fragment).
GN Name=Cngb1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
```

```
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Director MGC Project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045114; AAH45114.1; -.
DR HSSP; O88703; IQ43.
DR MGD; MGI:2664102; Cngblb.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; F: ion channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR InterPro; IPR00595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion Trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00442; CNMP_BINDING_3; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON TER 1
SQ SEQUENCE 866 AA; 97427 MW; CACC4AD8EB6DEE2A CRC64;

Query Match 100.0%; Score 110; DB 2; Length 866;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGNS 20
Db |||||
429 ASAFQIGSTHWYDGVGNS 448

RESULT 4
ID O35788 PRELIMINARY; PRT; 1339 AA.
AC O35788;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclic nucleotide-gated channel beta subunit.
GN Name=CNG4.1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sautter A., Biel M., Hofmann F.;
RT "Molecular cloning of cyclic nucleotide-gated cation channel subunits
RT from pineal gland.";
RL Mol. Brain Res. 47:171-175(1997).
DR EMBL; AJ000496; CAA04133.1; -.
DR HSSP; O88703; IQ43.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; F: ion channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR InterPro; IPR00595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion Trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00442; CNMP_BINDING_3; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 1339 AA; 151046 MW; FFAD64A6A81AB49A CRC64;

Query Match 100.0%; Score 110; DB 2; Length 1339;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGNS 20
Db 908 ASAFQIGSTHWYDGVGNS 927

RESULT 5
CNG4 HUMAN STANDARD; PRT; 909 AA.
AC Q14028; Q14029;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4)
DE (CNG4) (Cyclic nucleotide-gated cation channel modulatory subunit).
GN Name=CNGB1; Synonyms=CNGC4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RCNC2A AND RCNC2B).
RC TISSUE=Retina;
RX MEDLINE=93226050; PubMed=7682292; DOI=10.1038/362764a0;
RA Chen T.Y., Peng Y.-W., Dhallan R.S., Ahmed B., Reed R.R., Yau K.-W.;
RT "A new subunit of the cyclic nucleotide-gated cation channel in
retinal rods";
RL Nature 362:764-767(1993).
CC -!- SUBUNIT: Heterooligomeric complex with CNG1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RCNC2B;
CC IsoId=Q14028-1; Sequences=Displayed;
CC Name=RCNC2A;
CC IsoId=Q14028-2; Sequences=VSP 001110;
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(TC 1.A.1.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L15296; AAA65620.1; -;
CC EMBL; L15297; AAA65619.1; -;
CC Genew; HGNC:2151; CNGB1.
CC MIM; 600724; -;
CC DR GO; GO:0017071; C:intracellular cyclic nucleotide activated c. .; NAS.
CC DR GO; GO:005222; F:intracellular cAMP activated cation channel. .; NAS.
CC DR InterPro; IPR000595; cNMP binding.
CC DR InterPro; IPR005821; Ion trans.
CC DR InterPro; IPR001622; K+channel_pore.
CC Pfam; PF00027; cNMP binding; 1.
CC Pfam; PF00520; Ion trans; 1.
CC DR PROSITE; PS00888; cNMP BINDING 1; 1.
CC DR PROSITE; PS00889; cNMP BINDING 2; 1.
CC DR PROSITE; PS00442; cNMP BINDING 3; 1.
CC DR PROSITE; PS0042; cNMP BINDING 3; 1.
KW Alternative splicing; cAMP-binding; Ion transport; Ionic channel;
KW Multigene family; Transmembrane.
FT DOMAIN 1 314 Cytoplasmic (Potential).
FT TRANSMEM 315 333 H1 (Potential).
FT DOMAIN 334 347 Extracellular (Potential).
FT TRANSMEM 348 366 H2 (Potential).
FT DOMAIN 367 391 Cytoplasmic (Potential).
FT TRANSMEM 392 411 H3 (Potential).
FT DOMAIN 412 448 Extracellular (Potential).
FT TRANSMEM 449 471 H4 (Potential).

FT DOMAIN 472 515 Cytoplasmic (Potential).
FT TRANSMEM 516 535 H5 (Potential).
FT DOMAIN 536 619 Extracellular (Potential).
FT TRANSMEM 620 640 H6 (Potential).
FT DOMAIN 641 909 Cytoplasmic (Potential).
FT DOMAIN 9 29 Poly-Glu.
FT NP_BIND 628 767 CAMP (By similarity).
FT BINDING 688 688 CAMP (Potential).
FT BINDING 700 700 CAMP (Potential).
FT VARSPLIC 1 286 Missing (in isoform RCNC2A).
FT SEQUENCE 909 AA; 102285 MW; DC0E754336B6EDDD CRC64;
Query Match 95.5%; Score 105; DB 1; Length 909;
Best Local Similarity 90.0%; Pred. No. 4.5e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGNS 20
Db 470 ASAYQGLGSTHWYDGVGNS 489

RESULT 6
O43636 PRELIMINARY; PRT; 1245 AA.
AC O43636;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rod photoreceptor CNG-channel beta subunit.
GN Name=RCNC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Grunwald M.E., Yu W.P., Yu H.H., Yau K.W.;
RT "Identification of a domain on the beta subunit of the rod cGMP-gated
cation channel that mediates inhibition by calcium-calmodulin";
RL J. Biol. Chem. 267:10000-10006(1992).
DR EMBL; AF042498; AAC04830.1; -;
DR PIR; S32538; S32538.
DR PIR; S69275; S69275.
DR HSSP; O88703; 1043.
DR GO; GO:0015276; F:ligand-gated ion channel activity; TAS.
DR GO; GO:0006810; P:transport; TAS.
DR GO; GO:0007601; P:visual perception; TAS.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING 1; UNKNOWN_1.
DR PROSITE; PS00889; cNMP BINDING 2; 1.
DR PROSITE; PS00442; cNMP BINDING 3; 1.
DR PROSITE; PS0042; cNMP BINDING 3; 1.
KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
SQ SEQUENCE 1245 AA; 139159 MW; 40C4860BFCF86126 CRC64;
Query Match 95.5%; Score 105; DB 2; Length 1245;
Best Local Similarity 90.0%; Pred. No. 6.2e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGNS 20
Db 806 ASAYQGLGSTHWYDGVGNS 825

RESULT 7
Q9UNG2 PRELIMINARY; PRT; 1251 AA.
ID Q9UNG2
AC Q9UNG2;

QY 1 ASAFQIGSTHWYDGVGNS 20
||||:|||||||
Db 480 ASAYEGLGSTHWYDGVGNS 499

RESULT 10

O77660 ID O77660 PRELIMINARY; PRT; 952 AA.
AC O77660;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Cyclic nucleotide-gated channel beta subunit 1e.
GN Name=CNCbeta;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98345361; PubMed=9679145; DOI=10.1083/jcb.142.2.473;
RA Wiesner B., Weiner J., Miedendorff R., Hagen V., Kaupp U.B.,
RA Weyand I.;
RT "Cyclic nucleotide-gated channels on the flagellum control Ca2+ entry
RT into sperm.";
RL J. Cell Biol. 142:473-484(1998).
DR EMBL; AF074014; AAC26129.1; --
DR HSP; O88703; 1043.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; F: ion channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP BINDING 1; UNKNOWN_1.
DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR PROSITE; PS00442; cNMP BINDING_3; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 952 AA; 105913 MW; D43F8B1D27F7F052 CRC64;

Query Match 92.7%; Score 102; DB 2; Length 952;
Best Local Similarity 85.0%; Pred No. 1.3e-06;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGNS 20
||||:|||||||
Db 484 ASAYEGLGSTHWYDGVGNS 503

RESULT 11

CNG4_BOVIN ID CNG4_BOVIN STANDARD; PRT; 1394 AA.
AC 028181; Q03861; Q28082;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE 240 kDa protein of rod photoreceptor CNG-channel (Contains: Glutamic
DE acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4
DE (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel
DE modulatory subunit))1.
GN Name=CNGB1; Synonyms=CNG4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96009859; PubMed=7546742; DOI=10.1016/0896-6273(95)90151-5;

RA Koerschen H.G., Illing M., Seifert R., Sesti F., Williams A.,
RA Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
RA Kaupp U.B., Molday R.S.;
RT "A 240 kDa protein represents the complete beta subunit of the cyclic
RT nucleotide-gated channel from rod photoreceptor.";
RL Neuron 15:627-636(1995).
RN [2]
RP SEQUENCE OF 454-1394 FROM N.A. (ISOFORMS CNG4C; CNG4D AND CNG4E).
RC TISSUE=Testis;
RX MEDLINE=96198098; PubMed=8626431; DOI=10.1074/jbc.271.11.6349;
RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann E.;
RT "Molecular cloning and expression of the modulatory subunit of the
RT cyclic nucleotide-gated cation channel.";
RL J. Biol. Chem. 271:6349-6355(1996).
RN [3]
RP SEQUENCE OF 1-590 FROM N.A.
RC TISSUE=Retina;
RX PubMed=2014230;
RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
RT "The amino acid sequence of a glutamic acid-rich protein from bovine
RT retina as deduced from the cDNA sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3116-3119(1991).
CC 1- SUBUNIT: Forms functional heterooligomeric channels with CNG3.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Isoform CNG4D is the most frequent isoform
CC (CNG4D; CNG4C; CNG4E = 20:2:1) in testis;
CC Name=CNG4C;
CC IsoId=Q28181-1; Sequence=Displayed;
CC Name=CNG4D;
CC IsoId=Q28181-2; Sequence=VSP_001109;
CC Name=CNG4E;
CC IsoId=Q28181-3; Sequence=VSP_001108;
CC 1- TISSUE SPECIFICITY: Retina, testis, kidney, heart and brain.
CC 1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC 1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC EMBL; X89626; CAA61769.1; --
DR EMBL; X94707; CAA64367.1; --
DR EMBL; M61185; AAA30536.1; --
DR PIR; A40437; A40437.
DR Reactome; Q28181;
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion trans; 1.
DR PROSITE; PS00888; cNMP BINDING 1; 1.
DR PROSITE; PS00889; cNMP BINDING_2; 1.
DR PROSITE; PS00442; cNMP BINDING_3; 1.
KW Alternative splicing; cAMP-binding; Direct protein sequencing;
KW Ion transport; Ionic channel; Multigene family; Transmembrane.
FT CHAIN 1 590 Glutamic acid-rich protein.
FT DOMAIN 454 1394 Cyclic-nucleotide-gated cation channel 4.
FT TRANSMEM 771 789 Cytoplasmic (Potential).
FT DOMAIN 790 803 H1 (Potential).
FT TRANSMEM 804 822 Extracellular (Potential).
FT DOMAIN 823 847 H2 (Potential).
FT TRANSMEM 848 867 Cytoplasmic (Potential).
FT DOMAIN 868 904 H3 (Potential).
FT TRANSMEM 905 927 Extracellular (Potential).
FT DOMAIN 928 971 H4 (Potential).
FT TRANSMEM 972 991 Cytoplasmic (Potential).
FT H5 (Potential).

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FT DOMAIN 992 1075 Extracellular (Potential).
FT TRANSEM 1076 1096 H6 (Potential).
FT DOMAIN 1097 1394 Cytoplasmic (Potential).
FT NP_BIND 1084 1222 CAMP (By similarity).
FT BINDING 1144 1144 CAMP (Potential).
FT BINDING 1156 1156 CAMP (Potential).
FT CARBOHYD 1067 1067 N-linked (GlcNAc... ) (Potential).
FT VARSPPLIC 515 532 Missing (in isoform CNG4E).
FT VARSPPLIC 522 530 /FTId=VSP_001108.
FT VARSPPLIC 522 530 Missing (in isoform CNG4D).
FT CONFLICT 341 341 K -> E (in Ref. 3).
FT CONFLICT 454 465 REEEDDEEDD -> MRAGQKGR (in Ref. 2).
FT CONFLICT 482 482 R -> Q (in Ref. 2 and 3).
FT CONFLICT 499 499 A -> T (in Ref. 3).
FT CONFLICT 572 590 VPATEEPHELQVEDADADS -> GSFQMSPEALQCEALK
FT CONFLICT 1283 1283 S -> A (in Ref. 2).
FT CONFLICT 1289 1289 R -> A (in Ref. 2).
FT CONFLICT 1336 1336 D -> E (in Ref. 2).
FT CONFLICT 1338 1338 A -> AA (in Ref. 2).
SQ SEQUENCE 1394 AA; 155064 MW; EE6DA559BE3744A7 CRC64;

Query Match 92.7%; Score 102; DB 1; Length 1394;
Best Local Similarity 85.0%; Pred. No. 1.9e-06;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ASAFQGLGTHWYDGVGNS 20
Dbb 926 ASAYEGLGTHWYDGVGNS 945

RESULT 12
ID_CNB3_HUMAN STANDARD; PRT; 809 AA.
AC_O9NQW8; O9NRE9;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)
DE (Cyclic nucleotide-gated channel beta 3) (Cone photoreceptor cGMP-
DE gated channel beta subunit) (Cyclic nucleotide-gated cation channel
DE modulatory subunit).
DE Name=CNGB3;
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, VARIANT ACHM3
RP PHE-435, AND VARIANTS PRO-298 AND GLY-755.
RX MEDLINE=20414632; PubMed=10958649; DOI=10.1093/hmg/9.14.2107;
RA Kohl S., Baumann B., Broghammer M., Jaegle H., Sieving P., Kellner U.,
RA Spegal R., Anastasi M., Zrenner E., Sharpe L.T., Wässinger B.;
RT "Mutations in the CNGB3 gene encoding the beta-subunit of the cone
RT photoreceptor cGMP-gated channel are responsible for achromatopsia
RT (ACHM3) linked to chromosome 9Q21.";
RL Hum. Mol. Genet. 9:2107-2116(2000).
RL [2]
RP SEQUENCE OF 114-809 FROM N.A. (ISOFORM 2), FUNCTION, SUBUNIT, VARIANT
RP ACHM3 PHE-435, AND VARIANT CYS-234.
RC TISSE=Retina;
RX MEDLINE=20347712; PubMed=10888875; DOI=10.1038/77162;
RA Sundin O.H., Yang J.-M., Li Y., Zhu D., Hurd J.N., Mitchell T.N.,
RA Silva E.D., Maumenee I.H.;
RT "Genetic basis of total colourblindness among the Pingelapese
RT islanders.";
RL Nat. Genet. 25:289-293(2000).
CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
CC coupled cascade using cGMP as second messenger. This protein can
CC be activated by cGMP which leads to an opening of the cation
CC channel and thereby causing a depolarization of rod
CC photoreceptors. Induced a flickering channel gating, weakened the

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outward rectification in the presence of extracellular calcium,
increased sensitivity for L-cis diltiazem and enhanced the cAMP
efficiency of the channel when coexpressed with CNGA3 (By
similarity). Essential for the generation of light-evoked
electrical responses in the red-, green- and blue sensitive cones.
-!- SUBUNIT: Heterooligomeric complex with CNGA3.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
-!- Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=Q9NQW8-1; Sequence=Displayed;
Name=2;
IsoId=Q9NQW8-2; Sequence=VSP_009742;
Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Expressed specifically in the retina.
-!- DISEASE: Defects in CNGB3 are a cause of achromatopsia 3 (ACHM3)
[MIM:262300]; also known as Pingelapese blindness. ACHM3 is a
congenital complete achromatopsia and is distinct from total
colorblindness mainly because of the consistent concurrence of
severe myopia.
-!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
(TC 1.A.1.5) family.
-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
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EMBL; AF272900; AAF86274.1; -.
EMBL; AF228520; AAF80179.1; ALT_INIT.
Genew; HGNC:2153; CNGB3.
MIM; 605080; -.
MIM; 262300; -.
InterPro; IPR000595; cNMP_binding.
InterPro; IPR005821; Ion_trans.
InterPro; IPR001622; K_channel_pore.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; Ion_trans; 1.
SMART; SM00100; cNMP; 1.
PROSITE; PS00888; cNMP_BINDING_1; 1.
PROSITE; PS00889; cNMP_BINDING_2; 1.
PROSITE; PS00042; cNMP_BINDING_3; 1.
Alternative splicing; cGMP-binding; Disease mutation; Ion transport;
Ionic channel; Multigene family; Polymorphism; Transmembrane; Vision.
DOMAIN 1 216 Cytoplasmic (Potential).
TRANSEM 217 237 H1 (Potential).
DOMAIN 238 250 Extracellular (Potential).
TRANSEM 251 271 H2 (Potential).
DOMAIN 272 302 Cytoplasmic (Potential).
TRANSEM 303 323 H3 (Potential).
DOMAIN 324 359 Extracellular (Potential).
TRANSEM 360 380 H4 (Potential).
DOMAIN 381 417 Cytoplasmic (Potential).
TRANSEM 418 438 H5 (Potential).
DOMAIN 439 504 Extracellular (Potential).
TRANSEM 505 525 H6 (Potential).
DOMAIN 526 809 Cytoplasmic (Potential).
NP_BIND 532 576 cGMP (By similarity).
BINDING 592 592 cGMP (By similarity).
BINDING 604 604 cGMP (By similarity).
CARBOHYD 468 468 N-linked (GlcNAc... ) (Potential).
VARSPPLIC 590 594 Missing (in isoform 2).
FTId=VSP_009742.
VARIANT 234 234 W -> C (in dbSNP:6471482).
FTId=VAR_018109.
VARIANT 298 298 T -> P (in dbSNP:4961206).
FTId=VAR_018110.
VARIANT 435 435 S -> F (in ACHM3).
FTId=VAR_018111.

```

FT VARIANT 755 755 E -> G.
 FT SEQUENCE 809 AA; 92249 MW; AC23B7072C1C7DB3 CRC64;
 Query Match 70.0%; Score 77; DB 1; Length 809;
 Best Local Similarity 68.4%; Pred. No. 0.0065; 3; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGN 19
 || :|||:|||||
 Db 374 ASNYEGIGTRWYDGVGN 392

RESULT 13
 CNB3_MOUSE
 ID Q9JZ9; STANDARD; PRT; 694 AA.
 AC Q9JZ9;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cyclic nucleotide-gated cation channel beta 3 (CNG channel beta 3)
 DE Cyclic nucleotide-gated cation channel beta 3 (Cone photoreceptor cGMP-
 gated channel beta subunit) (Cyclic nucleotide-gated cation channel
 DE modulatory subunit) (Cyclic nucleotide-gated channel subunit CNGB3).
 GN Name=Cngb3; Synonyms=Cng6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6; TISSUE=Retina;
 RX MEDLINE=20130348; PubMed=10662822;
 RA Gerstner A., Zong X., Hofmann P., Biel M.;
 RT "Molecular cloning and functional characterization of a new modulatory
 cyclic nucleotide-gated channel subunit from mouse retina.";
 RL J. Neurosci. 20:1324-1332(2000).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 coupled cascade using cGMP as second messenger. This protein can
 be activated by cGMP which leads to an opening of the cation
 channel and thereby causing a depolarization of rod
 photoreceptors. Essential for the generation of light-evoked
 electrical responses in the red-, green- and blue sensitive cones
 (By similarity). Induced a flickering channel gating, weakened the
 outward rectification in the presence of extracellular calcium.
 CC increased sensitivity for L-cis diltiazem and enhanced the cAMP
 efficacy of the channel when coexpressed with CNGB3.
 CC -!- SUBUNIT: Heterooligomeric complex with CNGB3.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Small subset of retinal photoreceptor cells and
 testis.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC
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 CC
 CC EMBL; AJ243572; CAB71152.1; --
 CC MGD; MGI:1353562; Cngb3.
 CC GO; GO:0005886; C:plasma membrane; IC.
 CC GO; GO:0030553; F:3',5'-cGMP binding; IC.
 CC DR GO; GO:0005223; F:intracellular cGMP activated cation channel. .; IPI.
 CC GO; GO:0009187; P:cyclic nucleotide metabolism; IC.
 CC InterPro; IPR000595; cGMP binding.
 CC InterPro; IPR005821; Ion trans.
 CC DR InterPro; IPR001622; K:channel_pore.
 CC Pfam; PF00027; cGMP_binding; 1.

DR Pfam; PF00520; Ion trans; 1.
 DR SMART; SM00100; CNMP; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; 1.
 DR PROSITE; PS00889; CNMP_BINDING_2; 1.
 DR PROSITE; PS0042; CNMP_BINDING_3; 1.
 KW Cgmp-binding; Ion transport; Ionic channel; Multigene family;
 KW Transmembrane; Vision.
 FT DOMAIN 1 209
 FT TRANSMEM 210 230
 FT DOMAIN 231 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 294
 FT TRANSMEM 295 315
 FT DOMAIN 316 351
 FT TRANSMEM 352 372
 FT DOMAIN 373 409
 FT TRANSMEM 410 430
 FT DOMAIN 431 568
 FT TRANSMEM 569 589
 FT DOMAIN 590 694
 FT NP BIND 524 668
 FT BINDING 584 584
 FT BINDING 596 596
 FT CARBOHYD 507 507
 SQ SEQUENCE 694 AA; 79722 MW; 0B9F9CF3B180DA82 CRC64;
 Query Match 67.3%; Score 74; DB 1; Length 694;
 Best Local Similarity 68.4%; Pred. No. 0.016; 3; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASAFQIGSTHWYDGVGN 19
 || :|||:|||||
 Db 366 ASDYEGIGSTKWYNGEN 384

RESULT 14
 CNB3_CANFA
 ID Q8WJD7; STANDARD; PRT; 782 AA.
 AC Q8WJD7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cyclic nucleotide-gated cation channel beta 3 (CNG channel beta 3)
 DE Cyclic nucleotide-gated channel beta 3 (Cone photoreceptor cGMP-
 gated channel beta subunit) (Cyclic nucleotide-gated cation channel
 DE modulatory subunit).
 GN Name=CNGB3;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT CD ASN-262.
 RX PubMed=12140185; DOI=10.1093/hmg/11.16.1823;
 RA Sidjanin D.J., Lowe J.K., McElwee J.L., Milne B.S., Phippen T.M.,
 RA Saragan D.R., Aguirre G.D., Acland G.M., Ostrander E.A.;
 RT "Canine CNGB3 mutations establish cone degeneration as orthologous to
 the human achromatopsia locus ACHM3.";
 RL Hum. Mol. Genet. 11:1823-1833(2002).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 coupled cascade using cGMP as second messenger. This protein can
 be activated by cGMP which leads to an opening of the cation
 channel and thereby causing a depolarization of rod
 photoreceptors. Induced a flickering channel gating, weakened the
 outward rectification in the presence of extracellular calcium,
 CC increased sensitivity for L-cis diltiazem and enhanced the cAMP
 efficacy of the channel when coexpressed with CNGB3. Essential for
 the generation of light-evoked electrical responses in the red-,
 CC green- and blue sensitive cones (By similarity).
 CC -!- SUBUNIT: Heterooligomeric complex with CNGB3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DISEASE: Defects in CNGB3 are a cause of cone degeneration (cd).
 CC Cd is characterized by day-blindness and absence of retinal cone

function. This autosomal recessive disorder occurs naturally in the Alaskan Malamute and German Shorthaired Pointer breeds.

-1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.

-1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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EMBL; AF490511; AAM89224.1; -

DR InterPro; IPR000595; cNMP binding.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR001622; K-channel_pore.

DR Pfam; PF00027; cNMP binding; 1.

DR Pfam; PF00520; Ion_trans; 1.

DR SMART; SM00100; cNMP; 1.

DR PROSITE; PS00888; CNMP_BINDING_1; 1.

DR PROSITE; PS00889; CNMP_BINDING_2; 1.

DR PROSITE; PS00442; CNMP_BINDING_3; 1.

DR CGMP-binding; Disease mutation; Ion transport; Ionic channel;

KW Multigene family; Transmembrane; Vision.

FT DOMAIN 1 211 Cytoplasmic (Potential).

FT TRANSMEM 212 232 H1 (Potential).

FT DOMAIN 233 245 Extracellular (Potential).

FT TRANSMEM 246 266 H2 (Potential).

FT DOMAIN 267 297 Cytoplasmic (Potential).

FT TRANSMEM 298 318 H3 (Potential).

FT DOMAIN 319 412 Extracellular (Potential).

FT TRANSMEM 413 433 H4 (Potential).

FT DOMAIN 434 493 Cytoplasmic (Potential).

FT TRANSMEM 494 514 H5 (Potential).

FT DOMAIN 515 572 Extracellular (Potential).

FT TRANSMEM 573 593 H6 (Potential).

FT DOMAIN 594 782 Cytoplasmic (Potential).

FT NP_BIND 527 671 cGMP (By similarity).

FT BINDING 587 587 cGMP (By similarity).

FT BINDING 599 599 cGMP (By similarity).

FT VARIANT 262 262 D -> N (in cd; in a German Shorthaired Pointer).

SQ SEQUENCE 782 AA; 89424 MW; 7139EF3B86268A79 CRC64;

Query Match 67.3%; Score 74; DB 1; Length 782;

Best Local Similarity 68.4%; Pred. No. 0.018;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASAFQIGSTHWYDGVGN 19

Db 369 ASDVEGIGSTKWYNGGN 387

RESULT 15

Q95SL0 PRELIMINARY; PRT; 515 AA.

AC Q95SL0

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE GH17414p.

GN ORFNames=CG17922;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY060725; AAL28273.1; -

DR HSSP; O88703; 1Q3E

DR FlyBase; FBgn0034656; CG17922.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005216; F:ion channel activity; IEA.

DR GO; GO:0005267; F:potassium channel activity; IEA.

DR GO; GO:0006811; P:ion transport; IEA.

DR GO; GO:0006813; P:potassium ion transport; IEA.

DR InterPro; IPR000595; cNMP binding.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR001622; K-channel_pore.

DR Pfam; PF00027; cNMP binding; 1.

DR Pfam; PF00520; Ion_trans; 1.

DR SMART; SM00100; cNMP; 1.

DR PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.

DR PROSITE; PS00889; CNMP_BINDING_2; UNKNOWN_1.

DR PROSITE; PS00442; CNMP_BINDING_3; 1.

KW Ion transport; Ionic channel; Transmembrane; Transport.

SQ SEQUENCE 515 AA; 59084 MW; 35F58FC94343FBE2 CRC64;

Query Match 48.2%; Score 53; DB 2; Length 515;

Best Local Similarity 44.4%; Pred. No. 17;

Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SAFOGIGSTHWYDGVGN 19

Db 101 SDYQGLQNRWVSGKH 118

RESULT 16

Q9W2D5 PRELIMINARY; PRT; 1040 AA.

ID Q9W2D5; Q8IH43;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DB CG17922-PA (GH25102p).

GN ORFNames=CG17922;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mirza S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez K., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnikier S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003454; AAF46757.2; --
DR EMBL; BT001439; AANV1194.1; --
DR HSSP; O88703; 1Q3E.
DR FlyBase; FBgn0034656; CG17922.
GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; P:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR005821; ion_trans.
DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; cNMP_BINDING_2; UNKNOWN_1.
DR PROSITE; PS00422; cNMP_BINDING_3; 1.
KW ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 1040 AA; 118713 MW; 4A643FDA21D2D5B8 CRC64;

Query Match 48.2%; Score 53; DB 2; Length 1040;
Best Local Similarity 44.4%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SAFOGIGSTHWYDGVGN 19
Db 626 SDYQGLQGNRWVFGKGH 643

RESULT 17
Q38230 PRELIMINARY; PRT; 312 AA.
ID Q38230
AC Q38230;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Unidentified ORF35; putative; NCBI gi: 522255.
OS Lactococcus phage bIL67.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC c2-like viruses.
OX NCBI_TaxID=36343;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95111629; PubMed=7812447;
RA Schouler C., Ehrlich S.D., Chopin M.C.;
RT "Sequence and organization of the lactococcal prolate-headed bIL67
RL phage genome.";
RL Microbiology 140:3061-3069 (1994).
DR EMBL; L33769; AAA74324.1; --
DR InterPro; IPR008983; TNF-like.
SQ SEQUENCE 312 AA; 35662 MW; DF2A578502E57F6B CRC64;

Query Match 47.3%; Score 52; DB 2; Length 312;
Best Local Similarity 42.1%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SAFOGIGSTHWYDGVGN 20
Db 177 SNINGVGKTEWLKDSLGN 195

RESULT 18
Q858B2 PRELIMINARY; PRT; 333 AA.
ID Q858B2
AC Q858B2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF35.
OS Lactococcus phage bIL67.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC c2-like viruses.
OX NCBI_TaxID=36343;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22614033; PubMed=12726722; DOI=10.1016/S0042-6822(03)00012-6;
RA Stuer-Lauridsen B., Janzen T., Schnabl J., Johansen E.;

RT "Identification of the host determinant of two prolate-headed phages

RT infecting *Lactococcus lactis*."

RL Virology 309:10-17(2003).

DR EMBL; AY180212; AAO49840.1; -.

DR InterPro; IPR008983; TNF like.

SQ SEQUENCE 333 AA; 37924 MW; E68341237CCDBC6F CRC64;

Query Match 47.3%; Score 52; DB 2; Length 333;

Best Local Similarity 42.1%; Pred. No. 16;

Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SAFOGIGSTHWYDGVGNS 20

Db 177 SNINGVGKTEWLKDSLGNN 195

RESULT 19

Q845F2

ID Q845F2

AC Q845F2

DT 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Putative nitrous oxide reductase (Fragment).

GN Name=nosZ;

OS uncultured soil bacterium.

OC Bacteria; environmental samples.

OX NCBI_TaxID=164851;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;

RA Stres B., Manne I., Avgustin G., Tiedje J.M.;

RT "Nitrous oxide reductase (nosZ) gene fragments differ between native

RT and cultivated Michigan soils."

RL Appl. Environ. Microbiol. 70:301-309(2004).

DR EMBL; AJ550361; CAD79412.1; -.

DR HSP; Q51705; 1FWX.

DR InterPro; IPR011045; N2O_reductase_N.

DR NON TER 1

FT NON TER 375

SQ SEQUENCE 375 AA; 41875 MW; 389F4D4656101F5C CRC64;

Query Match 46.4%; Score 51; DB 2; Length 375;

Best Local Similarity 60.0%; Pred. No. 25;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGNS 20

Db 277 GLGPLHTAYDKGNS 291

RESULT 20

Q84XQ4

ID Q84XQ4

AC Q84XQ4

DT 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE NTPP27-like protein.

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamiales; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4113;

RN [1]

RP SEQUENCE FROM N.A.

RA Tian Z.D., Liu J., Xie C.H.;

RT "Cloning of a pathogenesis-related protein gene cDNA of potato using

RT RACE methods combined with cDNA library."

RL I Chuan Hsueh Pao 30:996-1002(2003).

DR EMBL; AY185207; AAO22065.1; -.

DR InterPro; IPR007541; BSP.

DR Pfam; PF04450; BSP; 1.

SQ SEQUENCE 226 AA; 25131 MW; 6FFFC0887BB81153 CRC64;

Query Match 45.5%; Score 50; DB 2; Length 226;

Best Local Similarity 57.1%; Pred. No. 21;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGN 19

Db 152 GLGFSHWKFGQGN 165

RESULT 21

Q687F6

ID Q687F6

AC Q687F6

DT 25-OCT-2004 (TRENBLrel. 28, Created)

DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)

DE Putative tail fiber component V.

GN ORFNames=EC_CPI639_53;

OS Bacteriophage CP-1639.

OC Viruses.

OX NCBI_TaxID=291401;

RN [1]

RP SEQUENCE FROM N.A.

RA Creuzburg K., Koehler B., Hempel H., Schreier P. Jacobs E.,

RT Schmidt H.;

RT "Genetic structure and chromosomal integration site of the cryptic

RT Shiga toxin 1-converting prophage CP-1639."

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Creuzburg K.;

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ304858; CAH23251.1; -.

DR InterPro; IPR003343; Big 2.

DR InterPro; IPR008964; Invasin_intimin.

DR Pfam; PF02368; Big 2; 1.

DR SMART; SM00635; BID 2; 1.

SQ SEQUENCE 250 AA; 26309 MW; A7D1CC7D7A5B257B CRC64;

Query Match 45.5%; Score 50; DB 2; Length 250;

Best Local Similarity 50.0%; Pred. No. 23;

Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QGIGSTHWYDGVGNS 20

Db 11 KGAGTTLWYNGKGA 26

RESULT 22

Q9EYD8

ID Q9EYD8

AC Q9EYD8

DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)

DE Major tail protein V (Hypothetical protein ECS2169) (Hypothetical

DE protein ECS2952) (Putative tail fiber component V of prophage Cp-

DE 933U).

GN OrderedLocusNames=ECS2169, ECS2952, Z3087;

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20564182; PubMed=11111050; DOI=10.1016/S0378-1119(00)00416-9;

RA Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,

RA Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Abe H., Iida T.,

RA Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,

RA Shinagawa H.;

RT "Complete nucleotide sequence of the defective Sakai-VT1 prophage


```
Query Match 44.5%; Score 49; DB 2; Length 245;
Best Local Similarity 53.3%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QIGSTHWYDGVGN 19
Db 11 KGAGTTLWYGTGD 25

RESULT 26
Q8FEW5 PRELIMINARY; PRT; 256 AA.
AC Q8FEW5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative tail component of prophage.
GN OrderedLocusNames=c3163;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6.H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rossch P.,
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016765; AA081615.1; -.
DR InterPro; IPR003343; Big 2.
DR Pfam; PF02368; Big 2; 1.
DR SMART; SM00635; BID_2; 1.
KW Complete proteome.
SQ SEQUENCE 256 AA; 26899 MW; 851E6ACFF831A4B6 CRC64;

Query Match 44.5%; Score 49; DB 2; Length 256;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QIGSTHWYDGVGN 19
Db 21 KGAGTTLWYNGSD 35

RESULT 27
Q845F4 PRELIMINARY; PRT; 375 AA.
AC Q845F4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ) gene fragments differ between native
RT and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309 (2004).
DR EMBL; AJ550359; CADW9410.1; -.
DR HSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1
```

```
FT NON_TER 375 375
SQ SEQUENCE 375 AA; 41882 MW; 6F8814654F962122 CRC64;

Query Match 44.5%; Score 49; DB 2; Length 375;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGNS 20
Db 277 GIGPLHTAYDGRGNA 291

RESULT 28
Q92VH1 PRELIMINARY; PRT; 387 AA.
ID Q92VH1;
AC Q92VH1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Putative calcium-binding exported protein.
GN ORFNames=SM021229;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OX Plasmid pSymb.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
DR EMBL; AL591985; CAC49133.1; -.
DR PIR; E95933; E95933.
GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001343; Hemlysn_Ca_bind.
DR InterPro; IPR011049; Serralysin_like_C.
DR Pfam; PF00353; HemolysinCabin; 14.
DR PRINTS; PR00313; CABNDNGRPT.
DR PROSITE; PS00330; HEMOLYSIN_CALCIIUM; 4.
KW Complete proteome; Plasmid.
SQ SEQUENCE 387 AA; 39371 MW; 5C597C2451A7E4D3 CRC64;

Query Match 44.5%; Score 49; DB 2; Length 387;
Best Local Similarity 47.1%; Pred. No. 51;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 3 AFQIGSTHWYDGVGN 19
Db 171 ALKQSGNDWYGGIGN 187

RESULT 29
Q8YP19 PRELIMINARY; PRT; 694 AA.
ID Q8YP19;
AC Q8YP19;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Translation elongation factor EF-G.
GN Name=fus; OrderedLocusNames=alr4383;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
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RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AF003596; BAB76082.1; --
 DR F01; AG2353; AG2353.
 DR HSP; P13551; 2EPG.
 DR GO; GO:0005525; F-GTP binding; IEA.
 DR GO; GO:0003746; P-translation elongation factor activity; IEA.
 DR GO; GO:0006412; P-protein biosynthesis; IEA.
 DR GO; GO:0006414; P-translational elongation; IEA.
 DR Pfam; PF00679; EFG C; 1.
 DR Pfam; PF03764; EFG IV; 1.
 DR Pfam; PF00009; GTP EFTU; 1.
 DR Pfam; PF03144; GTP EFTU D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRfam; TIGR00231; small_GTP; 1.
 KW Complete proteome; Elongation factor; GTP-binding.
 SQ SEQUENCE 694 AA; 76724 MW; B893DB6CDEEA4D3 CRC64;

Query Match 44.5%; Score 49; DB 2; Length 694;
 Match Local Similarity 70.0%; Pred. No. 89;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GIGSTHWYVD 15
 ID C1TC DROME STANDARD; PRT; 968 AA.
 DB 659 GVGSTFWAYD 668
 I:|:|:|:|:|

RESULT 30

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
 RX MEDLINE=99054704; PubMed=9832531;
 RA Rong Y.S., Golik K.G.;
 RT "Dominant defects in Drosophila eye pigmentation resulting from a
 RT euchromatin-heterochromatin fusion gene.";
 RL Genetics 150:1551-1566(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Fiankoc C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RL [3]
 RP GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [4]
 RP SEQUENCE OF 604-968 FROM N.A.
 RC STRAIN=Berkley; TISSUE=Head;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarini H., Kronmiller B., Pacieb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celisner S.E.;
 RA "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + NADP(+) =
 CC 5,10-methylenetetrahydrofolate + NADPH.
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + H(2)O = 10-
 CC formyltetrahydrofolate.
 CC -1- CATALYTIC ACTIVITY: ATP + formate + tetrahydrofolate = ADP +
 CC phosphate + 10-formyltetrahydrofolate.
 CC -1- PATHWAY: Necessary for the biosynthesis of purines, thymidylate,
 CC methionine, histidine, pantothenate, and formyl tRNA-Met.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=096553-1; Sequence=Displayed;
 CC Note=No experimental confirmation available;
 CC Name=A; Synonyms=C;
 CC IsoId=096553-2; Sequence=VSP_010883;
 CC -1- TISSUE SPECIFICITY: Present in all tissues.
 CC -1- MISCELLANEOUS: This trifunctional enzyme consists of two major
 CC domains: a N-terminal part, containing the methylene-THF
 CC dehydrogenase and the methenyl-THF cyclohydrolase activities and a
 CC larger formyl-THF synthetase domain.
 CC -1- SIMILARITY: In the N-terminal section; belongs to the
 CC tetrahydrofolate dehydrogenase/cyclohydrolase family.
 CC -1- SIMILARITY: In the C-terminal section; belongs to the formate--
 CC tetrahydrofolate ligase family.
 CC -----

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 CC or send an email to license@iesb-sib.ch).
 CC -----

DR EMBL; AF082097; AAC78847.1; -;
 DR EMBL; AE003688; AAG22140.2; -;
 DR EMBL; AE003688; AAN13478.1; -;
 DR EMBL; AY069146; AAL39291.1; ALT_INIT.
 DR HSP; P11586; 1A41.
 DR InAct; O96553; -;
 DR Flybase; FBgn020385; pug.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0004329; F:formate-tetrahydrofolate ligase activity; NAS.
 DR GO; GO:0004477; F:methylenetetrahydrofolate cyclohydrolase act. .; NAS.
 DR GO; GO:0004488; F:methylenetetrahydrofolate dehydrogenase (NA. .; NAS.
 DR GO; GO:0008652; F:amino acid biosynthesis; NAS.
 DR InterPro; IPR000559; Fmtcethd_synth.
 DR InterPro; IPR00672; THFDhg/Cyc_hydro.
 DR Pfam; PF01268; FTHFS; 1.
 DR Pfam; PF00763; THE_DHG_CYH; 1.
 DR Pfam; PF02882; THE_DHG_CYH_C; 1.
 DR PRINTS; PR00085; THFDHGNASE.
 DR PRODOM; PD002300; THFDhg/Cyc_hydro; 1.
 DR PROSITE; PS00721; FTHFS 1; 1.
 DR PROSITE; PS00722; FTHFS 2; FALSE_NEG.
 DR PROSITE; PS00766; THE_DHG_CYH 1; FALSE_NEG.
 DR PROSITE; PS00767; THE_DHG_CYH 2; 1.
 KW Alternative splicing; Amino-acid biosynthesis; ATP-binding;
 KW Histidine biosynthesis; Hydrolyase; Ligase; Methionine biosynthesis;
 KW Multifunctional enzyme; NADP; One-carbon metabolism; Oxidoreductase;
 KW Purine biosynthesis.
 FT DOMAIN 1 338 Methylenetetrahydrofolate dehydrogenase
 FT DOMAIN 339 968 and cyclohydrolase.
 FT NP_BIND 413 420 Formyltetrahydrofolate synthetase.
 FT VARSPIC 1 34 ATP (by similarity).
 FT /FTID=VSP 010883.
 SQ SEQUENCE 968 AA; 103503 MW; D65EC845DD8AF2C CRC64;

Query Match 44.5%; Score 49; DB 1; Length 968;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Oy 1 ASAFQIGSTHWYDVG 18
 Db 810 AGAFAAVSTHWADGGAG 827

RESULT 31
 Q7AEY8 PRELIMINARY; PRT; 246 AA.

AC Q7AEY8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Major tail protein.

CN OrderedLocusNames=ECG1640;

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;

RX MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murtata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 DR EMBL; AP002555; BAB35063.1; -;
 DR InterPro; IPR003343; Big 2.
 DR InterPro; IPR008964; Invasin_intimin.
 DR Pfam; PF02368; Big_2; 1.
 DR SMART; SM00635; BID_2; 1.
 SQ SEQUENCE 246 AA; 25761 MW; 46E7074462C6A57B CRC64;

Query Match 43.6%; Score 48; DB 2; Length 246;
 Best Local Similarity 53.3%; Pred. No. 46;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 5 QGIGSTHWYDVG 19
 Db 11 KGAGTTLWVYNGND 25

RESULT 32

Q8X6X3 PRELIMINARY; PRT; 256 AA.

ID Q8X6X3;
 AC Q8X6X3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative tail component of prophage CP-933X.
 CN OrderedLocusNames=z1894;
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glaesner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potanousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 DR EMBL; AE005331; AAG55990.1; -;
 DR PIR; B85691; B85691.
 DR PIR; H90833; H90833.
 DR Pfam; PF02368; Big_2; 1.
 DR SMART; SM00635; BID_2; 1.
 KW Complete proteome.

Query Match 43.6%; Score 48; DB 2; Length 256;
 Best Local Similarity 53.3%; Pred. No. 48;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 5 QGIGSTHWYDVG 19
 Db 21 KGAGTTLWVYNGND 35

RESULT 33

Q845F3 PRELIMINARY; PRT; 374 AA.

ID Q845F3;
 AC Q845F3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Putative nitrous oxide reductase (fragment).

CN Name=nos;

OS uncultured soil bacterium.

OC Bacteria; environmental samples.

OX NCBI_TaxID=164851;

```

[1]
RN SEQUENCE FROM N.A.
RP PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ), gene fragments differ between native
and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309(2004).
DR HSSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1 374
FT NON_TER 374 374
SQ SEQUENCE 374 AA; 41758 MW; 186CDD6B6501B62B CRC64;

Query Match 43.6%; Score 48; DB 2; Length 374;
Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291
|:| | | | | | | |
|:| | | | | | | |

RESULT 34
Q845F7 PRELIMINARY; PRT; 374 AA.
AC Q845F7
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ), gene fragments differ between native
and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309(2004).
DR HSSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1 374
FT NON_TER 374 374
SQ SEQUENCE 374 AA; 41972 MW; 3B2F164FA25526E8 CRC64;

Query Match 43.6%; Score 48; DB 2; Length 374;
Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291
|:| | | | | | | |
|:| | | | | | | |

RESULT 35
Q845D4 PRELIMINARY; PRT; 375 AA.
AC Q845D4
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;

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RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ), gene fragments differ between native
and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309(2004).
DR EMBL; AJ550353; CAD79568.1; -.
DR HSSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1 375
FT NON_TER 375 375
SQ SEQUENCE 375 AA; 42090 MW; 508608B3D2668C8E CRC64;

Query Match 43.6%; Score 48; DB 2; Length 375;
Best Local Similarity 53.3%; Pred. No. 70;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291
|:| | | | | | | |
|:| | | | | | | |

RESULT 36
Q845D9 PRELIMINARY; PRT; 375 AA.
AC Q845D9
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ), gene fragments differ between native
and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309(2004).
DR EMBL; AJ550374; CAD79425.1; -.
DR HSSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1 375
FT NON_TER 375 375
SQ SEQUENCE 375 AA; 42149 MW; 06CD3CF066376F1C CRC64;

Query Match 43.6%; Score 48; DB 2; Length 375;
Best Local Similarity 53.3%; Pred. No. 70;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291
|:| | | | | | | |
|:| | | | | | | |

RESULT 37
Q845F6 PRELIMINARY; PRT; 375 AA.
AC Q845F6
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ), gene fragments differ between native
and cultivated Michigan soils.";

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RL Appl. Environ. Microbiol. 70:301-309(2004).
DR EMBL; AJ550357; CAD79408.1; -.
DR HSSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1
SQ SEQUENCE 375 AA; 42047 MW; 635D2D0DB7B16B41 CRC64;

Query Match 43.6%; Score 48; DB 2; Length 375;
Best Local Similarity 53.3%; Pred. No. 70;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWVYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291

RESULT 38
Q845F8 PRELIMINARY; PRT; 375 AA.
ID Q845F8
AC Q845F8; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ) gene fragments differ between native
and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309(2004).
DR EMBL; AJ550355; CAD79406.1; -.
DR HSSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1
SQ SEQUENCE 375 AA; 42149 MW; 48AFD44CA199F9C1 CRC64;

Query Match 43.6%; Score 48; DB 2; Length 375;
Best Local Similarity 53.3%; Pred. No. 70;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWVYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291

RESULT 39
Q845G0 PRELIMINARY; PRT; 375 AA.
ID Q845G0
AC Q845G0; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ) gene fragments differ between native
and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309(2004).
DR EMBL; AJ550352; CAD79404.1; -.
DR HSSP; Q51705; 1FWX.
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DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1
SQ SEQUENCE 375 AA; 42051 MW; FE095211183EF778 CRC64;

Query Match 43.6%; Score 48; DB 2; Length 375;
Best Local Similarity 53.3%; Pred. No. 70;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWVYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291

RESULT 40
Q845G1 PRELIMINARY; PRT; 375 AA.
ID Q845G1
AC Q845G1; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Putative nitrous oxide reductase (Fragment).
GN Name=nosZ;
OS uncultured soil bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=164851;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14711656; DOI=10.1128/AEM.70.1.301-309.2004;
RA Stres B., Mahne I., Avgustin G., Tiedje J.M.;
RT "Nitrous oxide reductase (nosZ) gene fragments differ between native
and cultivated Michigan soils.";
RL Appl. Environ. Microbiol. 70:301-309(2004).
DR EMBL; AJ550351; CAD79403.1; -.
DR HSSP; Q51705; 1FWX.
DR InterPro; IPR011045; N2O_reductase_N.
FT NON_TER 1
SQ SEQUENCE 375 AA; 41994 MW; C261FDB236CAA153 CRC64;

Query Match 43.6%; Score 48; DB 2; Length 375;
Best Local Similarity 53.3%; Pred. No. 70;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GIGSTHWVYDGVGNS 20
Db 277 GLGPLHTAYDGKNA 291

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